STIC-Biotech/ChemLib 67100

From: Chan, Christina
Sent: Tuesday, May 21, 2002 1:35 PM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 09583848

Please rush. Thanks Chris

-----Original Message-----
From: Davis, Minh-Tam
Sent: Tuesday, May 21, 2002 12:03 PM
To: Chan, Christina
Subject: Rush search request for 09583848

Please use the parent case 08/037230 for searching.
Please search in commercial data base and in issued patent files:
Oligomer search for SEQ ID NO:18.
Since this case has priority date way back on 12/1991, is there anyway to print out sequences that are of older date?
Thanks.
MINH TAM DAVIS
ART UNIT 1642, ROOM 8A01, MB 8E12
305-2008

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

	TYPE OF SEARCH:	VENDOR/COST(where applic.)
Searcher: _____	NA Sequences:_____	STN: _____
Phone: _____	AA Sequences:_____	DIALOG: _____
Location: _____	Structures:_____	Questel/Orbit: _____
Date Picked Up: _____	Bibliographic: _____	DRLink:_____
Date Completed: _____	Litigation: _____	Lexis/Nexis: _____
Searcher Prep/Review: _____	Full text:_____	Sequence Sys.: _____
Clerical: _____	Patent Family:_____	WWW/Internet: _____
Online time: _____	Other:_____	Other (specify): _____

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U.S. DEPARTMENT OF COMMERCE
Patent and Trademark Office

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____

Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

STAFF USE ONLY

Date completed: 05-24-02
Searcher: Beverly C4994
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ Other CGN

PTO-1590 (9-90)

Davis, M.
08/037230
Seq. ID 18

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 01:35:51 ; Search time 1787.52 Seconds
(without alignments)
2634.080 Million cell updates/sec

Title: US-08-037-230D-18
Perfect score: 225
Sequence: 1 TATTTCTTTCCTGTGATCTT.....GCGACTGTGCCCCTGAGGAG 225

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	225	100.0	225	6	AR153509	AR153509 Sequence
2	225	100.0	225	6	I36933	I36933 Sequence 18
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5	157	69.8	1019	6	AR167377	AR167377 Sequence
6	157	69.8	1019	9	HUMMAGEB	D32076 Human mRNA
7	157	69.8	1362	6	AX019384	AX019384 Sequence
8	157	69.8	3871	9	HSU10691	U10691 Human MAGE-
9	157	69.8	245077	9	AF002997	AF002997 Homo sapi
10	74	32.9	1212	6	AX019380	AX019380 Sequence
11	74	32.9	1353	6	AX019376	AX019376 Sequence
12	74	32.9	1569	6	AX343855	AX343855 Sequence
13	74	32.9	1640	6	AR153502	AR153502 Sequence
14	74	32.9	1640	6	I36926	I36926 Sequence 11
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17	74	32.9	1710	9	BC017389	BC017389 Homo sapi
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19	74	32.9	1753	9	BC005963	BC005963 Homo sapi
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AC007040	Homo sapi
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AC107464	Homo sapi
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AL590429	Mouse DNA
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c 224	17	7.6	401	6	AX271708	AX271708 Sequence
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228	17	7.6	458	1	AF267547	AF267547 Escherich
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c 240	17	7.6	1625	5	XELXDLL	D10259 Xenopus mRN
c 241	17	7.6	1690	6	A87376	A87376 Sequence 7
c 242	17	7.6	1690	9	HSRNAULI4	Y10976 H.sapiens m
243	17	7.6	1824	9	HSUG2P	X01463 Human pseud
244	17	7.6	1947	6	AR153510	AR153510 Sequence
245	17	7.6	1947	6	I36934	I36934 Sequence 19
c 246	17	7.6	1955	9	AF234236S5	AF234241 Homo sapi
c 247	17	7.6	1973	1	D85898	D85898 Streptomyce
c 248	17	7.6	2038	10	AB024538	AB024538 Mus muscu
249	17	7.6	2116	9	AK055733	AK055733 Homo sapi
c 250	17	7.6	2163	10	AB024539	AB024539 Mus muscu
c 251	17	7.6	2402	9	HUM25DC1Z	L43411 Homo sapien
c 252	17	7.6	2441	9	AB060231	AB060231 Macaca fa
c 253	17	7.6	2699	9	AB006713	AB006713 Homo sapi
c 254	17	7.6	2929	9	AK057698	AK057698 Homo sapi
255	17	7.6	3001	6	AX194618	AX194618 Sequence
c 256	17	7.6	3346	1	PSU81032	U81032 Pseudomonas
257	17	7.6	3680	9	HSU10692	U10692 Human MAGE-
258	17	7.6	4986	9	AL662856	AL662856 Human DNA
259	17	7.6	5142	9	AY030237	AY030237 Homo sapi
260	17	7.6	5215	1	WSU131242	AJ131242 Wolinella
c 261	17	7.6	6156	9	HUM2OD8	D32063 Human gene
c 262	17	7.6	6210	9	AK024393	AK024393 Homo sapi
c 263	17	7.6	9566	1	RP1W17A	L40585 Xanthomonas
264	17	7.6	9995	1	AE008097	AE008097 Agrobacte
265	17	7.6	10184	9	AF410771	AF410771 Homo sapi
c 266	17	7.6	10585	2	AC110465	AC110465 Rattus no
c 267	17	7.6	10747	1	AE000406	AE000406 Escherich
268	17	7.6	11201	1	AE001732	AE001732 Thermotog
c 269	17	7.6	11365	9	AL591105	AL591105 Human DNA
270	17	7.6	11423	1	AE009132	AE009132 Agrobacte
c 271	17	7.6	11616	1	AE009767	AE009767 Pyrobacul
c 272	17	7.6	13847	9	HSL75B9B	Z69652 Human DNA s
273	17	7.6	14270	10	AF219626	AF219626 Mus muscu
274	17	7.6	14660	2	AC014636	AC014636 Drosophil
275	17	7.6	16043	9	HS360A4	AL031008 Human DNA
c 276	17	7.6	18700	9	AC078798	AC078798 Homo sapi
277	17	7.6	20539	9	HS349E10	AL022341 Human DNA
c 278	17	7.6	20873	9	AC079879	AC079879 Homo sapi
c 279	17	7.6	20890	9	HSU29895	U29895 Human 4-hyd
280	17	7.6	26078	9	AF376770	AF376770 Homo sapi
c 281	17	7.6	27846	9	AC092689	AC092689 Homo sapi
282	17	7.6	27900	2	AC109090	AC109090 Rattus no
c 283	17	7.6	28519	9	HSJ563E14	AL117379 Human DNA
284	17	7.6	29963	9	AL356859	AL356859 Human DNA
285	17	7.6	30500	9	AC013481	AC013481 Homo sapi
286	17	7.6	30895	2	AC067716	AC067716 Homo sapi
c 287	17	7.6	32874	3	AE003172	AE003172 Drosophil
c 288	17	7.6	33341	9	AC004750	AC004750 Homo sapi
289	17	7.6	33397	9	HSBA163M1	AL109802 Human DNA
c 290	17	7.6	33804	9	HS407A10	Z98883 Human DNA s
291	17	7.6	34768	9	AL138917	AL138917 Human DNA
292	17	7.6	35143	9	AP000229	AP000229 Homo sapi
293	17	7.6	35467	9	AC005570	AC005570 Homo sapi
c 294	17	7.6	35886	9	AC004035	AC004035 Homo sapi
295	17	7.6	36156	9	AC004789	AC004789 Homo sapi
296	17	7.6	36171	9	HSL219B8	Z54246 Human DNA s
c 297	17	7.6	36373	9	AL160252	AL160252 Human DNA
298	17	7.6	36630	9	AC006541	AC006541 Homo sapi
c 299	17	7.6	36700	9	AC004647	AC004647 Homo sapi
300	17	7.6	37139	9	AC006047	AC006047 Homo sapi
c 301	17	7.6	37248	9	AC096726	AC096726 Homo sapi
302	17	7.6	37425	3	U80842	U80842 Caenorhabdi
303	17	7.6	37428	2	AC026327	AC026327 Homo sapi
c 304	17	7.6	37990	3	CEC17G1	Z78415 Caenorhabdi
c 305	17	7.6	39608	9	AC009004	AC009004 Homo sapi
306	17	7.6	39756	9	HSL113B6	Z69837 Human DNA s
307	17	7.6	39850	5	FRU010348	AJ010348 Fugu rubr
308	17	7.6	40395	9	AC099491	AC099491 Homo sapi
c 309	17	7.6	40438	9	AC087410	AC087410 Homo sapi
c 310	17	7.6	40477	2	AC010514	AC010514 Homo sapi
c 311	17	7.6	40592	9	HSL191F1	Z68756 Human DNA s
c 312	17	7.6	40619	9	AC005222	AC005222 Homo sapi
c 313	17	7.6	40697	2	AC107874	AC107874 Homo sapi
c 314	17	7.6	41372	9	AL359082	AL359082 Human DNA
315	17	7.6	41459	9	AC004637	AC004637 Homo sapi
c 316	17	7.6	41618	9	AL355473	AL355473 Human DNA
317	17	7.6	41696	9	AC005932	AC005932 Homo sapi
c 318	17	7.6	42619	9	AC005615	AC005615 Homo sapi
319	17	7.6	43044	3	AC006730	AC006730 Caenorhab
320	17	7.6	43297	9	AC005578	AC005578 Homo sapi
c 321	17	7.6	43310	9	AC011519	AC011519 Homo sapi
322	17	7.6	43843	9	AC005796	AC005796 Homo sapi
323	17	7.6	43927	9	HSU69568	U69568 Human Xq28
c 324	17	7.6	44003	9	AF317635	AF317635 Homo sapi
325	17	7.6	44219	9	AC005512	AC005512 Homo sapi
c 326	17	7.6	44830	9	HSJ738A13	AL109801 Human DNA
327	17	7.6	44897	9	AF022794	AF022794 Homo sapi
328	17	7.6	45043	9	AF107045	AF107045 Homo sapi
c 329	17	7.6	45754	9	AL139118	AL139118 Human DNA
c 330	17	7.6	45966	2	AC092309	AC092309 Homo sapi
331	17	7.6	46463	9	HSE146D10	Z73420 Human DNA s
c 332	17	7.6	46508	9	AC073955	AC073955 Homo sapi
c 333	17	7.6	46619	9	AL513542	AL513542 Human DNA
c 334	17	7.6	46791	9	AC004699	AC004699 Homo sapi
335	17	7.6	48119	9	AL139190	AL139190 Human DNA
336	17	7.6	48478	2	AC026687	AC026687 Homo sapi
c 337	17	7.6	48763	9	AP000456	AP000456 Homo sapi
c 338	17	7.6	48860	9	AL136461	AL136461 Human DNA
339	17	7.6	50348	9	HS81G23	AL035459 Human DNA
c 340	17	7.6	51803	9	AF176815	AF176815 Homo sapi
c 341	17	7.6	51887	9	AL365193	AL365193 Human DNA
c 342	17	7.6	52378	2	AC100849	AC100849 Homo sapi
c 343	17	7.6	53000	2	AC003656_7	Continuation (8 of
c 344	17	7.6	53915	2	AC093147	AC093147 Homo sapi
345	17	7.6	54795	2	AC103701	AC103701 Homo sapi
346	17	7.6	54884	2	AC109519	AC109519 Homo sapi
347	17	7.6	55591	2	AC087813	AC087813 Homo sapi
348	17	7.6	56325	9	AL359712	AL359712 Human DNA
349	17	7.6	57759	9	AL137162	AL137162 Human DNA
c 350	17	7.6	59297	9	CNS07EG8	AL590327 Human chr
c 351	17	7.6	59378	2	AC100838	AC100838 Homo sapi
c 352	17	7.6	59765	9	AC005179	AC005179 Homo sapi
c 353	17	7.6	59816	2	AC107489	AC107489 Rattus no
c 354	17	7.6	60271	2	AC110286	AC110286 Homo sapi
355	17	7.6	60352	2	AC102868	AC102868 Mus muscu
c 356	17	7.6	60352	2	AC102868	AC102868 Mus muscu
357	17	7.6	61336	2	AC107802	AC107802 Mus muscu
358	17	7.6	61635	2	AC068928	AC068928 Homo sapi
359	17	7.6	62124	2	AC087580	AC087580 Homo sapi
c 360	17	7.6	62463	2	AC090300	AC090300 Homo sapi
c 361	17	7.6	63017	9	AL157710	AL157710 Human DNA
362	17	7.6	63681	9	AC079398	AC079398 Homo sapi
c 363	17	7.6	63906	2	AC090793	AC090793 Homo sapi
364	17	7.6	64114	2	AC084120	AC084120 Homo sapi
c 365	17	7.6	64829	2	AC100338	AC100338 Mus muscu

c 366	17	7.6	65882	9	AL589734	AL589734 Human DNA
c 367	17	7.6	66000	9	AL391119	AL391119 Human DNA
c 368	17	7.6	66126	2	AC100959	AC100959 Mus muscu
369	17	7.6	66206	2	AC023324	AC023324 Homo sapi
370	17	7.6	66748	2	AC090817	AC090817 Homo sapi
371	17	7.6	66817	9	AC005201	AC005201 Homo sapi
372	17	7.6	68369	9	AC093764	AC093764 Homo sapi
c 373	17	7.6	68476	2	AC021644_3	Continuation (4 of
374	17	7.6	68596	2	AC025118	AC025118 Homo sapi
375	17	7.6	68872	2	AC103726	AC103726 Homo sapi
c 376	17	7.6	68872	2	AC103726	AC103726 Homo sapi
c 377	17	7.6	69027	9	AL596306	AL596306 Human DNA
378	17	7.6	69238	2	AC090784	AC090784 Homo sapi
c 379	17	7.6	69479	9	AC008597	AC008597 Homo sapi
380	17	7.6	69535	9	AL583834	AL583834 Human DNA
381	17	7.6	69572	9	AC004769	AC004769 Homo sapi
c 382	17	7.6	71192	2	AC101620	AC101620 Mus muscu
383	17	7.6	71544	9	AC093792	AC093792 Homo sapi
384	17	7.6	71602	9	AC092105	AC092105 Homo sapi
385	17	7.6	71607	9	AC073184	AC073184 Homo sapi
c 386	17	7.6	71631	2	AC068525	AC068525 Homo sapi
387	17	7.6	73199	2	AC023017	AC023017 Homo sapi
388	17	7.6	73459	2	AC023557	AC023557 Homo sapi
c 389	17	7.6	74393	2	AC021587	AC021587 Homo sapi
390	17	7.6	75281	9	AL591893	AL591893 Human DNA
391	17	7.6	75525	9	AL391561	AL391561 Human DNA
392	17	7.6	76133	9	HSU71148	U71148 Human Xq28
393	17	7.6	76193	9	AL451081	AL451081 Human DNA
394	17	7.6	77087	9	AL355877	AL355877 Human DNA
c 395	17	7.6	77832	9	AL590039	AL590039 Human DNA
396	17	7.6	78220	2	AC023212	AC023212 Homo sapi
397	17	7.6	78941	9	AC005591	AC005591 Homo sapi
398	17	7.6	79061	2	AC021357	AC021357 Homo sapi
399	17	7.6	79170	9	AC026705	AC026705 Homo sapi
c 400	17	7.6	79237	9	HSDJ61M11	AL109624 Human DNA
c 401	17	7.6	79990	9	AC010457	AC010457 Homo sapi
402	17	7.6	80272	2	HSJ491C16	AL121976 Homo sapi
c 403	17	7.6	80824	9	AL513480	AL513480 Human DNA
c 404	17	7.6	81057	9	AC080125	AC080125 Homo sapi
c 405	17	7.6	81268	2	AC016408	AC016408 Homo sapi
c 406	17	7.6	81419	9	AL133382	AL133382 Human DNA
407	17	7.6	81786	9	AC003002	AC003002 Human DNA
408	17	7.6	81971	9	HS593C16	AL035702 Human DNA
c 409	17	7.6	82183	9	HSJ1037B9	AL117377 Human DNA
c 410	17	7.6	84335	2	AC018387	AC018387 Homo sapi
c 411	17	7.6	84570	9	AL359552	AL359552 Human DNA
c 412	17	7.6	84707	9	AL355475	AL355475 Human DNA
413	17	7.6	84879	9	AL590325	AL590325 Human DNA
414	17	7.6	85084	9	AB042297	AB042297 Homo sapi
415	17	7.6	86381	2	AL360077	AL360077 Homo sapi
c 416	17	7.6	86554	2	AC090280	AC090280 Homo sapi
c 417	17	7.6	86829	9	AC011382	AC011382 Homo sapi
418	17	7.6	87156	2	AC068450	AC068450 Homo sapi
419	17	7.6	87434	9	HSA297357	AJ297357 Homo sapi
420	17	7.6	87739	2	AL592150	AL592150 Homo sapi
421	17	7.6	87789	9	AL133270	AL133270 Human DNA
422	17	7.6	87925	9	AC005318	AC005318 Homo sapi
423	17	7.6	87944	2	AC023662	AC023662 Homo sapi
424	17	7.6	88071	9	AC002316	AC002316 Homo sapi
425	17	7.6	88473	9	AF191071	AF191071 Homo sapi
426	17	7.6	88718	2	AC097545	AC097545 Rattus no
427	17	7.6	89044	2	AC099680	AC099680 Homo sapi
c 428	17	7.6	89448	9	AC005067	AC005067 Homo sapi
429	17	7.6	89665	9	AC063976	AC063976 Homo sapi
c 430	17	7.6	89862	9	AC007164	AC007164 Homo sapi
431	17	7.6	90399	2	AL162405	AL162405 Homo sapi
432	17	7.6	91355	9	AL391417	AL391417 Human DNA
433	17	7.6	91365	9	HS116F5	Z93244 Human DNA s
434	17	7.6	92569	9	AL353688	AL353688 Human DNA
435	17	7.6	92636	9	AC005251	AC005251 Homo sapi
c 436	17	7.6	92679	2	AC098804	AC098804 Homo sapi
437	17	7.6	93033	2	AP000644	AP000644 Homo sapi
438	17	7.6	93567	2	AP004179	AP004179 Oryza sat
c 439	17	7.6	93923	2	AC090818	AC090818 Homo sapi
c 440	17	7.6	94524	2	AC022115	AC022115 Homo sapi
441	17	7.6	95655	2	AC110069	AC110069 Homo sapi
c 442	17	7.6	96157	9	AL138789	AL138789 Human DNA
443	17	7.6	96532	9	CNS07EG6	AL590079 Human chr
c 444	17	7.6	97101	2	AL450308	AL450308 Homo sapi
c 445	17	7.6	97687	9	AL591403	AL591403 Human DNA
c 446	17	7.6	97749	9	AC004906	AC004906 Homo sapi
447	17	7.6	98247	2	AC025777	AC025777 Homo sapi
c 448	17	7.6	98247	2	AC025777	AC025777 Homo sapi
449	17	7.6	99594	2	AF263284	AF263284 Homo sapi
450	17	7.6	99595	9	AL513283	AL513283 Human DNA
c 451	17	7.6	99682	9	HS452H17	Z96810 Human DNA s
452	17	7.6	99864	2	AC023489	AC023489 Trypanoso
453	17	7.6	100000	9	AP000144	AP000144 Homo sapi
454	17	7.6	100000	9	AP000498	AP000498 Homo sapi
455	17	7.6	100000	9	AP000509	AP000509 Homo sapi
456	17	7.6	100000	9	AP000513	AP000513 Homo sapi
c 457	17	7.6	100116	9	AL591178	AL591178 Human DNA
458	17	7.6	100167	9	HSJ189G13	AL121916 Human DNA
c 459	17	7.6	100375	9	HS193B12	Z98744 Human DNA s
460	17	7.6	100634	9	AP001594	AP001594 Homo sapi
461	17	7.6	101670	2	AC105714	AC105714 Rattus no
462	17	7.6	102308	9	AC005231	AC005231 Homo sapi
c 463	17	7.6	102387	9	AC022114	AC022114 Homo sapi
c 464	17	7.6	102567	2	AC027694	AC027694 Homo sapi
465	17	7.6	102624	9	AL161912	AL161912 Human DNA
466	17	7.6	103565	9	AC005022	AC005022 Homo sapi
467	17	7.6	103606	9	AC005004	AC005004 Homo sapi
c 468	17	7.6	103720	9	AL161717	AL161717 Human DNA
c 469	17	7.6	104309	9	AL138717	AL138717 Human DNA
470	17	7.6	104357	9	AL392123	AL392123 Human DNA
471	17	7.6	104660	9	AP000347	AP000347 Homo sapi
472	17	7.6	104871	9	AC004584	AC004584 Homo sapi
c 473	17	7.6	105065	2	AC069132	AC069132 Homo sapi
c 474	17	7.6	105118	9	AC019127	AC019127 Homo sapi
475	17	7.6	105138	9	AF124730	AF124730 Homo sapi
476	17	7.6	105272	9	AL671884	AL671884 Human DNA
c 477	17	7.6	105563	9	AC003983	AC003983 Human PAC
478	17	7.6	106441	9	HSJ803J11	AL117350 Human DNA
479	17	7.6	106795	9	AC004864	AC004864 Homo sapi
480	17	7.6	107104	9	HS1179L24	AL096708 Human DNA
c 481	17	7.6	107480	9	AC073118	AC073118 Homo sapi
c 482	17	7.6	107603	9	HS934G17	AL021155 Homo sapi
483	17	7.6	108373	9	AL358034	AL358034 Human DNA
c 484	17	7.6	108793	9	AL137839	AL137839 Human DNA
485	17	7.6	108845	1	U66917	U66917 Pseudomonas
c 486	17	7.6	108902	2	AC011430	AC011430 Homo sapi
c 487	17	7.6	108922	9	AC016870	AC016870 Homo sapi
488	17	7.6	109176	9	AL161911	AL161911 Human DNA
c 489	17	7.6	109867	9	AC004898	AC004898 Homo sapi
c 490	17	7.6	110000	1	ECOUW67_2	Continuation (3 of
c 491	17	7.6	110000	2	AC003656_6	Continuation (7 of
492	17	7.6	110000	2	AC105291_1	Continuation (2 of
c 493	17	7.6	110000	2	AL139235_2	Continuation (3 of
c 494	17	7.6	110000	2	AL354714_5	Continuation (6 of
495	17	7.6	110000	2	AL354792_0	AL354792 Homo sapi
496	17	7.6	110000	2	AL670455_3	Continuation (4 of
c 497	17	7.6	110013	2	AC046157	AC046157 Homo sapi
c 498	17	7.6	110535	9	AC005091	AC005091 Homo sapi
c 499	17	7.6	110716	2	AC008717	AC008717 Homo sapi
c 500	17	7.6	110820	9	AL596285	AL596285 Human DNA
c 501	17	7.6	110965	9	AC026697	AC026697 Homo sapi
c 502	17	7.6	111037	2	AC090067	AC090067 Homo sapi
c 503	17	7.6	111076	2	AP003162	AP003162 Homo sapi
504	17	7.6	111118	9	HSAC000112	AC000112 Human PAC
505	17	7.6	111560	9	AC016940	AC016940 Homo sapi
c 506	17	7.6	113019	2	AC090141	AC090141 Homo sapi
c 507	17	7.6	113212	9	AL513355	AL513355 Human DNA
c 508	17	7.6	113879	9	AC011904	AC011904 Homo sapi
509	17	7.6	113929	9	AF196969	AF196969 Homo sapi
510	17	7.6	113982	2	AF192303	AF192303 Homo sapi
c 511	17	7.6	114149	9	AC022083	AC022083 Homo sapi

512	17	7.6	114434	9	AC093728	AC093728 Homo sapi
513	17	7.6	115408	2	AC068848	AC068848 Homo sapi
c 514	17	7.6	116014	9	AL353772	AL353772 Human DNA
c 515	17	7.6	116079	9	AL365271	AL365271 Human DNA
c 516	17	7.6	116368	9	HS1112F19	AL034420 Human DNA
c 517	17	7.6	116513	9	HS487J7	AL008730 Human DNA
518	17	7.6	116664	9	HS1191N16	AL118501 Human DNA
c 519	17	7.6	117521	2	AC023784	AC023784 Homo sapi
c 520	17	7.6	117911	9	HS117P19	Z86061 Human DNA s
c 521	17	7.6	118030	2	AP000667	AP000667 Homo sapi
c 522	17	7.6	118068	9	AL356798	AL356798 Human DNA
523	17	7.6	118153	9	HS249C1	AL022154 Human DNA
524	17	7.6	118440	9	AC016939	AC016939 Homo sapi
525	17	7.6	118447	2	AC093508	AC093508 Homo sapi
c 526	17	7.6	118447	2	AC093508	AC093508 Homo sapi
c 527	17	7.6	118492	2	AC020548	AC020548 Homo sapi
528	17	7.6	118499	9	AL390722	AL390722 Human DNA
529	17	7.6	118906	9	AL353583	AL353583 Human DNA
c 530	17	7.6	118995	9	AC005368	AC005368 Homo sapi
c 531	17	7.6	119235	2	AC011817	AC011817 Homo sapi
532	17	7.6	119296	9	CNS05TEX	AL359402 Human chr
c 533	17	7.6	119395	9	AL139189	AL139189 Human DNA
c 534	17	7.6	119460	9	AL590431	AL590431 Human DNA
c 535	17	7.6	119502	9	AL157781	AL157781 Human DNA
c 536	17	7.6	120134	2	AC008034	AC008034 Homo sapi
c 537	17	7.6	120466	9	AC093813	AC093813 Homo sapi
c 538	17	7.6	120871	9	AP001054	AP001054 Homo sapi
c 539	17	7.6	121212	9	HS135L22	AL031767 Human DNA
540	17	7.6	121700	9	AC007622	AC007622 Homo sapi
541	17	7.6	121788	2	AC022420	AC022420 Homo sapi
542	17	7.6	121800	9	AL359924	AL359924 Human DNA
543	17	7.6	121949	9	AL157772	AL157772 Human DNA
544	17	7.6	122001	2	AC107375	AC107375 Homo sapi
545	17	7.6	122102	9	AC010468	AC010468 Homo sapi
546	17	7.6	122103	9	HS291J10	Z93017 Human DNA s
547	17	7.6	122302	9	AC003982	AC003982 Homo sapi
c 548	17	7.6	122638	9	AB001523	AB001523 Homo sapi
c 549	17	7.6	122717	2	AP001186	AP001186 Homo sapi
c 550	17	7.6	122913	9	AL139404	AL139404 Human DNA
c 551	17	7.6	123062	2	AC099359	AC099359 Rattus no
552	17	7.6	123170	2	AL138792	AL138792 Homo sapi
553	17	7.6	123507	2	AC099721	AC099721 Homo sapi
554	17	7.6	123554	9	AB023049	AB023049 Homo sapi
555	17	7.6	123631	9	HS22F01	AL109967 Homo sapi
c 556	17	7.6	123693	9	AL162853	AL162853 Human DNA
557	17	7.6	123778	9	AC069294	AC069294 Homo sapi
558	17	7.6	123830	9	HS500L14	AL023583 Human DNA
559	17	7.6	124001	9	HS886K2	AL031295 Human DNA
560	17	7.6	124437	9	AL139125	AL139125 Human DNA
561	17	7.6	124635	9	AP000593	AP000593 Homo sapi
c 562	17	7.6	124699	9	AL590617	AL590617 Human DNA
563	17	7.6	124975	2	AC107063	AC107063 Bos tauru
c 564	17	7.6	125291	9	AP000646	AP000646 Homo sapi
c 565	17	7.6	125553	9	AL513263	AL513263 Human DNA
c 566	17	7.6	125746	9	AC010589	AC010589 Homo sapi
c 567	17	7.6	126807	9	HS391O22	AL031577 Human DNA
568	17	7.6	127145	9	HS1119A7	AL022313 Human DNA
c 569	17	7.6	127905	9	AL513550	AL513550 Human DNA
570	17	7.6	128435	9	AL590411	AL590411 Human DNA
571	17	7.6	128683	2	AF286886	AF286886 Homo sapi
c 572	17	7.6	128769	2	AL139261	AL139261 Homo sapi
c 573	17	7.6	129011	2	AC091860	AC091860 Homo sapi
c 574	17	7.6	129048	9	AC020931	AC020931 Homo sapi
575	17	7.6	129169	2	AC032038	AC032038 Homo sapi
c 576	17	7.6	129225	9	AC026765	AC026765 Homo sapi
c 577	17	7.6	129504	9	AL445469	AL445469 Human DNA
578	17	7.6	129727	9	AC084381	AC084381 Homo sapi
579	17	7.6	129949	2	AC022940	AC022940 Homo sapi
c 580	17	7.6	129949	2	AC022940	AC022940 Homo sapi
c 581	17	7.6	130639	9	AL356489	AL356489 Human DNA
c 582	17	7.6	130647	9	AL157385	AL157385 Human DNA
c 583	17	7.6	130715	9	AL391557	AL391557 Human DNA
c 584	17	7.6	130754	2	AC008508	AC008508 Homo sapi
585	17	7.6	131274	9	AC069506	AC069506 Homo sapi
c 586	17	7.6	131928	9	AC091738	AC091738 Homo sapi
587	17	7.6	132068	9	AC006965	AC006965 Homo sapi
c 588	17	7.6	132327	9	AL158209	AL158209 Human DNA
c 589	17	7.6	132433	9	HSDJ210B1	AL078593 Human DNA
590	17	7.6	133687	2	AC002093	AC002093 Homo sapi
591	17	7.6	133786	9	AC091839	AC091839 Homo sapi
c 592	17	7.6	133814	2	AC027550	AC027550 Homo sapi
c 593	17	7.6	133922	9	AC023469	AC023469 Homo sapi
594	17	7.6	133965	9	AF064861	AF064861 Homo sapi
595	17	7.6	134184	9	AC095044	AC095044 Homo sapi
c 596	17	7.6	134347	9	AL356295	AL356295 Human DNA
c 597	17	7.6	134882	9	AC008622	AC008622 Homo sapi
c 598	17	7.6	134890	2	AC009793	AC009793 Homo sapi
c 599	17	7.6	135405	9	AC000025	AC000025 Homo sapi
600	17	7.6	135637	9	AP003400	AP003400 Homo sapi
601	17	7.6	135648	9	AC004069	AC004069 Homo sapi
c 602	17	7.6	135666	2	AL513013	AL513013 Homo sapi
c 603	17	7.6	136105	2	AC100740	AC100740 Mus muscu
604	17	7.6	136168	9	HS1049G11	AL078634 Human DNA
605	17	7.6	136587	9	AL445309	AL445309 Human DNA
606	17	7.6	136778	2	AC108376	AC108376 Pan trogl
607	17	7.6	136932	9	AC068035	AC068035 Homo sapi
c 608	17	7.6	137271	9	AC004552	AC004552 Homo sapi
609	17	7.6	137610	9	AC013478	AC013478 Homo sapi
610	17	7.6	137730	9	HS365E2	AL009177 Human DNA
611	17	7.6	137737	9	AC010378	AC010378 Homo sapi
c 612	17	7.6	137833	9	CNS01DV6	AL133455 Human chr
c 613	17	7.6	137886	30	AC027581	Ac027581 Homo sapi
614	17	7.6	137950	9	AC022137	AC022137 Homo sapi
615	17	7.6	138021	9	AC090820	AC090820 Homo sapi
c 616	17	7.6	138224	9	AC096562	AC096562 Homo sapi
617	17	7.6	138329	2	AC093226-	AC093226 Homo sapi
618	17	7.6	138725	2	AC012031	AC012031 Homo sapi
619	17	7.6	138752	9	AL161627	AL161627 Human DNA
620	17	7.6	139607	2	AC104796	AC104796 Homo sapi
621	17	7.6	139627	9	AL357117	AL357117 Human DNA
622	17	7.6	140007	2	AC091896	AC091896 Homo sapi
c 623	17	7.6	140242	2	AC073038	AC073038 Homo sapi
c 624	17	7.6	140292	9	CNS01DU8	AL133223 Human chr
625	17	7.6	140334	9	AC021802	AC021802 Homo sapi
626	17	7.6	140378	2	AC068205	AC068205 Homo sapi
627	17	7.6	140403	2	AC109444	AC109444 Homo sapi
c 628	17	7.6	140706	2	AC098106	AC098106 Rattus no
c 629	17	7.6	140874	2	AC027227	AC027227 Homo sapi
c 630	17	7.6	140944	2	AC096136	AC096136 Rattus no
c 631	17	7.6	140974	9	AC068533	AC068533 Homo sapi
c 632	17	7.6	141371	9	AC010319	AC010319 Homo sapi
633	17	7.6	141372	2	AC011779	AC011779 Homo sapi
634	17	7.6	141701	2	AC024541	AC024541 Homo sapi
c 635	17	7.6	141779	9	AC002377	AC002377 Human PAC
636	17	7.6	142123	2	AC068890	AC068890 Homo sapi
c 637	17	7.6	142215	2	AC092066	AC092066 Homo sapi
638	17	7.6	142254	2	AC094110	AC094110 Pan trogl
639	17	7.6	142277	2	AC016204	AC016204 Homo sapi
640	17	7.6	142441	2	HSJ344H20	AL132710 Homo sapi
641	17	7.6	142494	9	AL137119	AL137119 Human DNA
c 642	17	7.6	142669	2	AC018912	AC018912 Homo sapi
c 643	17	7.6	142805	9	AL592525	AL592525 Human DNA
c 644	17	7.6	142933	9	AL513102	AL513102 Human DNA
c 645	17	7.6	142938	2	AC104184	AC104184 Homo sapi
c 646	17	7.6	143163	9	HSBK21C21	AL049861 Human DNA
647	17	7.6	143428	9	AL162587	AL162587 Human DNA
648	17	7.6	143436	9	AC004456	AC004456 Homo sapi
c 649	17	7.6	143591	2	AC092197	AC092197 Homo sapi
650	17	7.6	143676	2	AC026435	AC026435 Homo sapi
651	17	7.6	143683	9	AL356376	AL356376 Human DNA
c 652	17	7.6	143754	2	AL359093	AL359093 Homo sapi
653	17	7.6	143840	30	AC027210	Ac027210 Homo sapi
654	17	7.6	143893	2	AC010766	AC010766 Homo sapi
655	17	7.6	143952	9	AL589987	AL589987 Human DNA
656	17	7.6	144233	2	AC068103	AC068103 Homo sapi
c 657	17	7.6	144494	2	AC099534	AC099534 Homo sapi

c 658	17	7.6 144542	9	AC015819	AC015819	Homo sapi
659	17	7.6 144555	2	AC037451	AC037451	Homo sapi
c 660	17	7.6 144676	9	HS390O13	Z84469	Human DNA s
661	17	7.6 144967	2	AC008963	AC008963	Homo sapi
c 662	17	7.6 145100	2	AC024641	AC024641	Homo sapi
663	17	7.6 145101	2	AC021775	AC021775	Homo sapi
664	17	7.6 145152	2	AC005805	AC005805	Homo sapi
c 665	17	7.6 145253	9	AC006329	AC006329	Homo sapi
c 666	17	7.6 145329	2	AC055850	AC055850	Homo sapi
667	17	7.6 145414	9	HS78F24	AL022336	Human DNA
668	17	7.6 145414	9	HSA392M18	AL121897	Human DNA
c 669	17	7.6 145414	9	HSA392M18	AL121897	Human DNA
c 670	17	7.6 145442	9	AC004859	AC004859	Homo sapi
c 671	17	7.6 145630	9	AL512622	AL512622	Human DNA
c 672	17	7.6 145831	6	AX330137	AX330137	Sequence
c 673	17	7.6 145831	6	AX334634	AX334634	Sequence
c 674	17	7.6 145831	6	AX336416	AX336416	Sequence
c 675	17	7.6 145831	6	AX337041	AX337041	Sequence
c 676	17	7.6 145831	9	HUAF001548	AF001548	Human Chr
c 677	17	7.6 146124	9	AL358938	AL358938	Human DNA
c 678	17	7.6 146278	9	AL356413	AL356413	Human DNA
c 679	17	7.6 146312	2	AC008769	AC008769	Homo sapi
c 680	17	7.6 146677	2	AC016275	AC016275	Homo sapi
681	17	7.6 146776	2	AC093486	AC093486	Homo sapi
c 682	17	7.6 146805	2	AL450424	AL450424	Homo sapi
c 683	17	7.6 147259	2	AC019248	AC019248	Homo sapi
684	17	7.6 147260	2	AC016340	AC016340	Homo sapi
c 685	17	7.6 147260	2	AC016340	AC016340	Homo sapi
c 686	17	7.6 147964	2	AC008158	AC008158	Homo sapi
c 687	17	7.6 148018	2	HSDJ613A2	AL121990	Homo sapi
688	17	7.6 148049	9	HSA300188	AJ300188	Homo sapi
689	17	7.6 148081	9	AB045361	AB045361	Homo sapi
690	17	7.6 148164	2	AC105105	AC105105	Homo sapi
c 691	17	7.6 148430	9	AL139328	AL139328	Human DNA
c 692	17	7.6 148487	2	AC011583	AC011583	Homo sapi
693	17	7.6 148507	9	AC008784	AC008784	Homo sapi
c 694	17	7.6 148507	9	AC008784	AC008784	Homo sapi
695	17	7.6 148598	9	HSBA51C14	AL121875	Human DNA
c 696	17	7.6 148653	2	AC110281	AC110281	Homo sapi
697	17	7.6 148752	9	AL596225	AL596225	Human DNA
698	17	7.6 148772	2	AC055826	AC055826	Homo sapi
c 699	17	7.6 149133	2	AC079089	AC079089	Homo sapi
700	17	7.6 149202	2	AC022160	AC022160	Homo sapi
c 701	17	7.6 149214	2	AC026535	AC026535	Homo sapi
c 702	17	7.6 149308	9	AC005527	AC005527	Homo sapi
703	17	7.6 149321	9	HS106I20	AL079295	Human DNA
c 704	17	7.6 149409	9	AC004081	AC004081	Homo sapi
705	17	7.6 149618	9	AP000556	AP000556	Homo sapi
c 706	17	7.6 149705	9	AC074362	AC074362	Homo sapi
707	17	7.6 149901	2	AC068563	AC068563	Homo sapi
c 708	17	7.6 150036	9	AP000557	AP000557	Homo sapi
709	17	7.6 150193	2	AC009641	AC009641	Homo sapi
710	17	7.6 150332	9	AC004921	AC004921	Homo sapi
c 711	17	7.6 150354	9	AC091920	AC091920	Homo sapi
712	17	7.6 150520	9	AL136305	AL136305	Human DNA
c 713	17	7.6 150581	9	AP003693	AP003693	Homo sapi
714	17	7.6 150587	2	AC005973	AC005973	Homo sapi
c 715	17	7.6 150759	2	AP001130	AP001130	Homo sapi
c 716	17	7.6 150855	2	AC021258	AC021258	Homo sapi
c 717	17	7.6 150896	2	AC098980	AC098980	Rattus no
718	17	7.6 150902	2	AC018391	AC018391	Homo sapi
c 719	17	7.6 150947	2	AC087370	AC087370	Homo sapi
720	17	7.6 151008	2	AC035146	AC035146	Homo sapi
c 721	17	7.6 151008	2	AC035146	AC035146	Homo sapi
722	17	7.6 151026	9	AC005915	AC005915	Homo sapi
723	17	7.6 151182	9	AL611942	AL611942	Human DNA
c 724	17	7.6 151228	9	AL662800	AL662800	Human DNA
c 725	17	7.6 151294	2	AC069364	AC069364	Homo sapi
c 726	17	7.6 151341	2	AC019297	AC019297	Homo sapi
c 727	17	7.6 151552	9	AL355863	AL355863	Human DNA
c 728	17	7.6 151736	2	AC024439	AC024439	Homo sapi
729	17	7.6 151801	9	AC008906	AC008906	Homo sapi
730	17	7.6 151881	9	AC008629	AC008629	Homo sapi
c 731	17	7.6 152058	2	AC025232	AC025232	Homo sapi
c 732	17	7.6 152224	2	AC007933	AC007933	Homo sapi
733	17	7.6 152269	2	AL591024	AL591024	Homo sapi
734	17	7.6 152573	9	AL445202	AL445202	Human DNA
735	17	7.6 152583	9	HSDJ534K7	AL109925	Human DNA
736	17	7.6 152659	9	AL591503	AL591503	Human DNA
737	17	7.6 152664	2	AC012158	AC012158	Homo sapi
c 738	17	7.6 152861	2	AC023451	AC023451	Homo sapi
739	17	7.6 153088	2	AC046135	AC046135	Homo sapi
740	17	7.6 153094	2	AC096715	AC096715	Homo sapi
c 741	17	7.6 153108	9	AL355273	AL355273	Human DNA
742	17	7.6 153154	2	AL669876	AL669876	Homo sapi
c 743	17	7.6 153168	9	AC011974	AC011974	Homo sapi
c 744	17	7.6 153218	2	AC015920	AC015920	Homo sapi
745	17	7.6 153241	9	AC023510	AC023510	Homo sapi
746	17	7.6 153381	2	AP001990	AP001990	Homo sapi
747	17	7.6 153392	9	AL133548	AL133548	Human DNA
748	17	7.6 153539	2	AL591168	AL591168	Homo sapi
749	17	7.6 153629	9	AC092325	AC092325	Homo sapi
750	17	7.6 153778	2	AC087528	AC087528	Homo sapi
751	17	7.6 153860	2	AC016301	AC016301	Homo sapi
752	17	7.6 154036	9	AC008068	AC008068	Homo sapi
c 753	17	7.6 154323	2	AC026033	AC026033	Homo sapi
754	17	7.6 154394	9	HS34B21	AL031778	Human DNA
c 755	17	7.6 154453	2	AC018533	AC018533	Homo sapi
756	17	7.6 154499	2	AC031987	AC031987	Homo sapi
757	17	7.6 154526	2	AL592111	AL592111	Homo sapi
c 758	17	7.6 154584	2	AC015641	AC015641	Homo sapi
759	17	7.6 154597	9	AP004295	AP004295	Homo sapi
c 760	17	7.6 154616	2	AC067772	AC067772	Homo sapi
c 761	17	7.6 154664	9	AC025362	AC025362	Homo sapi
c 762	17	7.6 154744	2	AC079114	AC079114	Homo sapi
763	17	7.6 154897	2	AC060762	AC060762	Homo sapi
c 764	17	7.6 154904	9	AL162272	AL162272	Human DNA
765	17	7.6 155022	9	AC002395	AC002395	Homo sapi
c 766	17	7.6 155053	2	AC015795	AC015795	Homo sapi
767	17	7.6 155106	2	AC104069	AC104069	Homo sapi
c 768	17	7.6 155186	2	AC068373	AC068373	Homo sapi
769	17	7.6 155195	2	AC092518	AC092518	Felis cat
770	17	7.6 155332	2	AC040900	AC040900	Homo sapi
c 771	17	7.6 155405	9	AC009812	AC009812	Homo sapi
c 772	17	7.6 155667	2	AC067911	AC067911	Homo sapi
773	17	7.6 155770	2	AC092381	AC092381	Homo sapi
774	17	7.6 155816	2	AC091927	AC091927	Homo sapi
775	17	7.6 155824	2	AC087296	AC087296	Homo sapi
c 776	17	7.6 156277	9	AC026795	AC026795	Homo sapi
777	17	7.6 156371	2	AC104116	AC104116	Homo sapi
778	17	7.6 156386	2	AC009171	AC009171	Homo sapi
779	17	7.6 156473	2	AC097261	AC097261	Homo sapi
780	17	7.6 156481	2	AL392107	AL392107	Homo sapi
781	17	7.6 156542	9	AC018618	AC018618	Homo sapi
782	17	7.6 156596	2	AL445070	AL445070	Homo sapi
783	17	7.6 156700	2	AC027051	AC027051	Homo sapi
784	17	7.6 156733	9	AP000640	AP000640	Homo sapi
785	17	7.6 156748	2	AC015481	AC015481	Homo sapi
786	17	7.6 156833	9	AC018712	AC018712	Homo sapi
c 787	17	7.6 156836	2	AC068059	AC068059	Homo sapi
788	17	7.6 157007	2	AC066599	AC066599	Homo sapi
c 789	17	7.6 157023	2	AC107018	AC107018	Homo sapi
c 790	17	7.6 157067	9	AC010163	AC010163	Homo sapi
791	17	7.6 157086	9	AP000552	AP000552	Homo sapi
c 792	17	7.6 157116	9	AC009054	AC009054	Homo sapi
793	17	7.6 157225	2	AC105765	AC105765	Homo sapi
794	17	7.6 157321	9	AC004912	AC004912	Homo sapi
795	17	7.6 157336	2	AC079787	AC079787	Homo sapi
c 796	17	7.6 157337	9	AC009163	AC009163	Homo sapi
c 797	17	7.6 157390	2	AC025366	AC025366	Homo sapi
c 798	17	7.6 157402	2	AC034161	AC034161	Homo sapi
c 799	17	7.6 157463	9	AC091529	AC091529	Homo sapi
c 800	17	7.6 157478	2	AC015515	AC015515	Homo sapi
801	17	7.6 157548	2	AC026637	AC026637	Homo sapi
c 802	17	7.6 157565	2	AL160156	AL160156	Homo sapi
803	17	7.6 157657	2	AC074243	AC074243	Homo sapi

804	17	7.6	157662	9	AL139035	AL139035 Human DNA
c 805	17	7.6	157779	9	AL590624	AL590624 Human DNA
c 806	17	7.6	157813	9	AC005535	AC005535 Homo sapi
c 807	17	7.6	157814	2	AC037460	AC037460 Homo sapi
808	17	7.6	157819	30	Al160277	Al160277 Human DNA
809	17	7.6	157834	2	AC022931	AC022931 Homo sapi
810	17	7.6	157872	9	AC007850	AC007850 Homo sapi
c 811	17	7.6	158073	9	AC069298	AC069298 Homo sapi
c 812	17	7.6	158099	9	CNS05TBU	AL352955 Human chr
813	17	7.6	158214	9	CNS05TC0	AL352981 Human chr
c 814	17	7.6	158338	2	AC024720	AC024720 Homo sapi
c 815	17	7.6	158427	9	AC002553	AC002553 Homo sapi
c 816	17	7.6	158591	9	AC010188	AC010188 Homo sapi
c 817	17	7.6	158700	2	AC027643	AC027643 Homo sapi
818	17	7.6	158898	9	U82696	U82696 Homo sapien
c 819	17	7.6	158902	2	AC013778	AC013778 Homo sapi
c 820	17	7.6	159013	2	AP000931	AP000931 Homo sapi
821	17	7.6	159057	2	AC023995	AC023995 Homo sapi
822	17	7.6	159110	9	AL355296	AL355296 Human DNA
823	17	7.6	159146	2	AL592424	AL592424 Homo sapi
824	17	7.6	159209	2	AC079097	AC079097 Homo sapi
825	17	7.6	159254	2	AC084394	AC084394 Homo sapi
826	17	7.6	159273	2	AC025001	AC025001 Homo sapi
827	17	7.6	159294	9	AL357506	AL357506 Human DNA
828	17	7.6	159366	2	AC073595	AC073595 Homo sapi
c 829	17	7.6	159409	2	AC092900	AC092900 Homo sapi
830	17	7.6	159433	2	AC021859	AC021859 Homo sapi
c 831	17	7.6	159516	2	AC048350	AC048350 Homo sapi
c 832	17	7.6	159610	2	AC012137	AC012137 Homo sapi
833	17	7.6	159692	2	AC013693	AC013693 Homo sapi
834	17	7.6	159698	9	AC027269	AC027269 Homo sapi
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836	17	7.6	159723	2	AC021862	AC021862 Homo sapi
837	17	7.6	159765	2	AL359533	AL359533 Mus muscu
c 838	17	7.6	160015	9	AC092183	AC092183 Homo sapi
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863	17	7.6	161445	2	AP000938	AP000938 Homo sapi
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874	17	7.6	161987	9	AC006070	AC006070 Homo sapi
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900	17	7.6	163392	9	AL589765	AL589765 Human DNA
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902	17	7.6	163521	2	AC108040	AC108040 Homo sapi
903	17	7.6	163599	9	HSDJ81D8	AL109933 Human DNA
904	17	7.6	163632	9	AL513185	AL513185 Human DNA
c 905	17	7.6	163660	2	AC046165	AC046165 Homo sapi
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c 907	17	7.6	163807	2	AC018934	AC018934 Homo sapi
908	17	7.6	163828	2	AL662867	AL662867 Homo sapi
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910	17	7.6	164028	9	AC004890	AC004890 Homo sapi
911	17	7.6	164144	9	AL591704	AL591704 Human DNA
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916	17	7.6	164479	9	AC103922	AC103922 Homo sapi
c 917	17	7.6	164485	2	AC025340	AC025340 Homo sapi
918	17	7.6	164500	2	AL359698	AL359698 Homo sapi
c 919	17	7.6	164508	2	AC104130	AC104130 Homo sapi
920	17	7.6	164519	9	AL138712	AL138712 Human DNA
c 921	17	7.6	164522	9	AC026191	AC026191 Homo sapi
922	17	7.6	164601	2	AC104476	AC104476 Pan trogl
c 923	17	7.6	164632	2	AC025624	AC025624 Homo sapi
924	17	7.6	164651	2	AC020994	AC020994 Homo sapi
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932	17	7.6	165617	9	CNS0000K	AL049840 Human chr
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935	17	7.6	165994	9	AC090509	AC090509 Homo sapi
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938	17	7.6	166178	2	AP002990	AP002990 Homo sapi
c 939	17	7.6	166192	9	AC096737	AC096737 Homo sapi
c 940	17	7.6	166233	2	AC048369	AC048369 Homo sapi
c 941	17	7.6	166237	9	AL139379	AL139379 Human DNA
c 942	17	7.6	166336	2	AC007716	AC007716 Homo sapi
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c 949	17	7.6	166731	9	AC093910	AC093910 Homo sapi

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951	17	7.6	166758	2	AC024428	AC024428 Homo sapi
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c 953	17	7.6	166970	2	AC094775	AC094775 Rattus no
954	17	7.6	167022	9	AC010238	AC010238 Homo sapi
c 955	17	7.6	167080	9	AC007014	AC007014 Homo sapi
c 956	17	7.6	167101	9	AC002094	AC002094 Genomic s
957	17	7.6	167124	2	AC091559	AC091559 Homo sapi
958	17	7.6	167292	2	AC068365	AC068365 Homo sapi
c 959	17	7.6	167343	6	AX332231	AX332231 Sequence
c 960	17	7.6	167343	6	AX335067	AX335067 Sequence
c 961	17	7.6	167343	9	HSU96629	U96629 Human chrom
c 962	17	7.6	167398	9	CNS07EET	AL445886 Human chr
c 963	17	7.6	167429	2	AC099394	AC099394 Homo sapi
c 964	17	7.6	167477	9	AL442643	AL442643 Human DNA
965	17	7.6	167498	2	AP000750	AP000750 Homo sapi
c 966	17	7.6	167522	2	AC097004	AC097004 Papio cyn
c 967	17	7.6	167563	9	AC069280	AC069280 Homo sapi
c 968	17	7.6	167570	9	AC092668	AC092668 Homo sapi
c 969	17	7.6	167687	2	AC023476	AC023476 Homo sapi
970	17	7.6	167863	2	AL590651	AL590651 Homo sapi
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c 972	17	7.6	167998	9	AL353662	AL353662 Human DNA
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975	17	7.6	168145	9	AL159171	AL159171 Human DNA
976	17	7.6	168154	2	AC016456	AC016456 Homo sapi
c 977	17	7.6	168168	2	AC012283	AC012283 Homo sapi
978	17	7.6	168258	2	AC018703	AC018703 Homo sapi
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c 980	17	7.6	168425	2	AC012198	AC012198 Homo sapi
981	17	7.6	168467	9	AL450346	AL450346 Human DNA
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c 983	17	7.6	168473	2	AC063917	AC063917 Homo sapi
c 984	17	7.6	168509	2	AC015570	AC015570 Homo sapi
985	17	7.6	168648	2	AC096892	AC096892 Rattus no
986	17	7.6	168659	2	AL359883	AL359883 Homo sapi
987	17	7.6	168710	2	AP000894	AP000894 Homo sapi
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c 990	17	7.6	168872	9	AC073325	AC073325 Homo sapi
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993	17	7.6	168937	2	AC018747	AC018747 Homo sapi
c 994	17	7.6	169103	2	AC025687	AC025687 Homo sapi
995	17	7.6	169118	2	AC096645	AC096645 Homo sapi
c 996	17	7.6	169234	9	CNS06C7Q	AL390799 Human chr
997	17	7.6	169235	2	AC026224	AC026224 Homo sapi
998	17	7.6	169323	2	AL161906	AL161906 Homo sapi
999	17	7.6	169370	2	AC022954	AC022954 Homo sapi
1000	17	7.6	169374	2	AC026050	AC026050 Homo sapi

ALIGNMENTS

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RESULT   1
AR153509
LOCUS       AR153509                 225 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 18 from patent US 6235525.
ACCESSION   AR153509
VERSION     AR153509.1  GI:15121041
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 225)
  AUTHORS   van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.
  TITLE     Isolated nucleic acid molecules coding for tumor rejection antigen
            precursor MAGE-3 and uses thereof
  JOURNAL   Patent: US 6235525-A 18 22-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .225
                     /organism="unknown"
BASE COUNT       44 a      65 c      58 g      58 t
ORIGIN


  Query Match             100.0%;  Score 225;  DB 6;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-121;
  Matches  225;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TATTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
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Db       1 TATTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60

Qy      61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120

Qy     121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAGGACAGGCTTCCTGATAATC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAGGACAGGCTTCCTGATAATC 180

Qy     181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCTGAGGAG 225
           |||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCTGAGGAG 225


RESULT   2
I36933
LOCUS       I36933                   225 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 18 from patent US 5612201.
ACCESSION   I36933
VERSION     I36933.1  GI:2084893
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 225)
  AUTHORS   De Plaen,E., Boon-Falleur,T., Lethe,B., Szikora,J.-P., De Smet,C.
            and Chomez,P.
  TITLE     Isolated nucleic acid molecules useful in determining expression of
            a tumor rejection antigen precursor
  JOURNAL   Patent: US 5612201-A 18 18-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .225
                     /organism="unknown"
BASE COUNT       44 a      65 c      58 g      58 t
ORIGIN


  Query Match             100.0%;  Score 225;  DB 6;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-121;
  Matches  225;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TATTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
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Db       1 TATTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60

Qy      61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120

Qy     121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAGGACAGGCTTCCTGATAATC 180
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Db     121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAGGACAGGCTTCCTGATAATC 180

Qy     181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCTGAGGAG 225
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Db     181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCTGAGGAG 225


RESULT   3
AR167371
LOCUS       AR167371                 945 bp    DNA     linear   PAT 17-DEC-2001
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DEFINITION  Sequence 7 from patent US 6287569.
ACCESSION   AR167371
VERSION     AR167371.1  GI:17903147
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 945)
  AUTHORS   Kipps,T.J. and Wu,Y.
  TITLE     Vaccines with enhanced intracellular processing
  JOURNAL   Patent: US 6287569-A 7 11-SEP-2001;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
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ORIGIN


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  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
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Db    496 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 555

Qy    124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
          |||||||||||||||||||||||||||||||||||||
Db    556 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 592


RESULT   4
HSU10339
LOCUS       HSU10339                 945 bp    mRNA    linear   PRI 13-JUN-1994
DEFINITION  Human MAGE-3b mRNA, complete cds.
ACCESSION   U10339
VERSION     U10339.1  GI:499121
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 945)
  AUTHORS   Fenton,R.G.
  TITLE     Cloning and Analysis of MAGE-1 Related Genes
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 945)
  AUTHORS   Fenton,R.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUN-1994) Robert G. Fenton, BRMP, NCI-FCRDC,
            Frederick, MD 21702, USA
FEATURES             Location/Qualifiers
     source          1. .945
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                     /db_xref="taxon:9606"
                     /clone="MAGE-3b"
                     /haplotype="HLA-A1/A2"
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                     /cell_type="melanoma"
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                     /dev_stage="adult"
                     /note="cancer patient"
     CDS             1. .945
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                     /product="MAGE-3b"
                     /protein_id="AAA19006.1"
                     /db_xref="GI:499122"
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                     LVEVTLGEVPAAESPDPPQSPQGASSLPTTMNYPLWSQSYEDSSNQEEEGPSTFPDLE
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                     VFGIELMEVDPIGHVYIFATCLGLSYDGLLGDNQIMPKTGFLIIILAIIAKEGDCAPE
                     EKIWEELSVLEVFEGREDSIFGDPKKLLTQYFVQENYLEYRQVPGSDPACYEFLWGPR
                     ALIETSYVKVLHHMVKISGGPRISYPLLHEWALREGEE"
BASE COUNT      213 a    254 c    275 g    203 t
ORIGIN


  Query Match             69.8%;  Score 157;  DB 9;  Length 945;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-81;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
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Db    496 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 555

Qy    124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
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Db    556 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 592


RESULT   5
AR167377
LOCUS       AR167377                 1019 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 13 from patent US 6287569.
ACCESSION   AR167377
VERSION     AR167377.1  GI:17903153
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   Kipps,T.J. and Wu,Y.
  TITLE     Vaccines with enhanced intracellular processing
  JOURNAL   Patent: US 6287569-A 13 11-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .1019
                     /organism="unknown"
BASE COUNT      224 a    284 c    292 g    219 t
ORIGIN


  Query Match             69.8%;  Score 157;  DB 6;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-81;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
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Db    501 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 560

Qy     64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    561 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 620

Qy    124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
          |||||||||||||||||||||||||||||||||||||
Db    621 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 657


RESULT   6
HUMMAGEB
LOCUS       HUMMAGEB                 1019 bp    mRNA    linear   PRI 07-FEB-1999
DEFINITION  Human mRNA for MAGE-6 potein, complete cds.
ACCESSION   D32076
VERSION     D32076.1  GI:1125015
KEYWORDS    MAGE-6 protein; melanoma antigen.
SOURCE      Homo sapiens cell-line M73 cDNA to mRNA.
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   Imai,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JUL-1994) Yasuhisa Imai, Kurume University School of
            Medicine, Immunology; Asahi 67, Kurume, Fukuoka 830, Japan
            (Tel:0942-31-7551, Fax:0942-31-7699)
REFERENCE   2  (bases 1 to 1019)
  AUTHORS   Imai,Y., Shichijo,S., Yamada,A., Katayama,T., Yano,H. and Itoh,K.
  TITLE     Sequence analysis of the MAGE gene family encoding human
            tumor-rejection antigens
  JOURNAL   Gene 160 (2), 287-290 (1995)
  MEDLINE   95369706
FEATURES             Location/Qualifiers
     source          1. .1019
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /cell_line="M73"
     CDS             66. .1010
                     /standard_name="melanoma antigen-6"
                     /note="Nomenclature of MAGE-6 was according to MAGE gene's
                     27 nucletide sequences of HLA-A1 binding motif (Traversari
                     etc., 1992)"
                     /codon_start=1
                     /evidence=experimental
                     /product="MAGE-6 protein"
                     /protein_id="BAA06842.1"
                     /db_xref="GI:1125016"
                     /translation="MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAASSSST
                     LVEVTLGEVPAAESPDPPQSPQGASSLPTTMNYPLWSQSYEDSSNQEEEGPSTFPDLE
                     SEFQAALSRKVAKLVHFLLLKYRAREPVTKAEMLGSVVGNWQYFFPVIFSKASDSLQL
                     VFGIELMEVDPIGHVYIFATCLGLSYDGLLGDNQIMPKTGFLIIILAIIAKEGDCAPE
                     EKIWEELSVLEVFEGREDSIFGDPKKLLTQYFVQENYLEYRQVPGSDPACYEFLWGPR
                     ALIETSYVKVLHHMVKISGGPRISYPLLHEWALREGEE"
BASE COUNT      224 a    284 c    292 g    219 t
ORIGIN


  Query Match             69.8%;  Score 157;  DB 9;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-81;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 560

Qy     64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    561 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 620

Qy    124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
          |||||||||||||||||||||||||||||||||||||
Db    621 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 657


RESULT   7
AX019384
LOCUS       AX019384                1362 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 10 from Patent WO9940188.
ACCESSION   AX019384
VERSION     AX019384.1  GI:10043354
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1362)
  AUTHORS   Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.
  TITLE     Tumor-associated antigen derivatives from the mage family, and
            nucleic acid sequences encoding them, used for the preparation of
            fusion proteins and of compositions for vaccination
  JOURNAL   Patent: WO 9940188-A 10 12-AUG-1999;
            SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
            JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)
FEATURES             Location/Qualifiers
     source          1. .1362
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /note="Melanoma tissue"
BASE COUNT      345 a    348 c    383 g    286 t
ORIGIN


  Query Match             69.8%;  Score 157;  DB 6;  Length 1362;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-81;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    826 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 885

Qy     64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    886 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 945

Qy    124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
          |||||||||||||||||||||||||||||||||||||
Db    946 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 982


RESULT   8
HSU10691
LOCUS       HSU10691                3871 bp    DNA     linear   PRI 23-JUN-1995
DEFINITION  Human MAGE-6 antigen (MAGE6) gene, complete cds.
ACCESSION   U10691
VERSION     U10691.1  GI:533522
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3871)
  AUTHORS   De Plaen,E., Arden,K., Traversari,C., Gaforio,J.J., Szikora,J.P.,
            De Smet,C., Brasseur,F., van der Bruggen,P., Lethe,B.,
            Lurquin,C.Brasseur.R., Chomez,P., De Backer,O., Cavenee,W. and
            Boon,T.
  TITLE     Structure, chromosomal localization, and expression of 12 genes of
            the MAGE family
  JOURNAL   Immunogenetics 40 (5), 360-369 (1994)
  MEDLINE   95012457
REFERENCE   2  (bases 1 to 3871)
  AUTHORS   De Plaen,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-1994) Etienne De Plaen, Ludwig Institute for
            Cancer Research, 74 Avenue Hippocrate, Brussels, 1200, Belgium
FEATURES             Location/Qualifiers
     source          1. .3871
                     /organism="Homo sapiens"
                     /isolate="patient MZ2"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /sex="female"
                     /cell_type="lymphocyte"
                     /tissue_type="blood"
                     /dev_stage="adult"
     exon            2053. .2118
                     /number=2
     exon            2199. .>3762
                     /number=3
     gene            2264. .3208
                     /gene="MAGE6"
     CDS             2264. .3208
                     /gene="MAGE6"
                     /codon_start=1
                     /product="MAGE-6 antigen"
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                     /protein_id="AAA68875.1"
                     /db_xref="GI:533523"
                     /translation="MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAASSSST
                     LVEVTLGEVPAAESPDPPQSPQGASSLPTTMNYPLWSQSYEDSSNQEEEGPSTFPDLE
                     SEFQAALSRKVAKLVHFLLLKYRAREPVTKAEMLGSVVGNWQYFFPVIFSKASDSLQL
                     VFGIELMEVDPIGHVYIFATCLGLSYDGLLGDNQIMPKTGFLIIILAIIAKEGDCAPE
                     EKIWEELSVLEVFEGREDSIFGDPKKLLTQYFVQENYLEYRQVPGSDPACYEFLWGPR
                     ALIETSYVKVLHHMVKISGGPRISYPLLHEWALREGEE"
BASE COUNT      865 a    1050 c    1117 g     839 t
ORIGIN


  Query Match           69.8%;  Score 157;  DB 9;  Length 3871;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-81;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2699 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 2758

Qy      64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2759 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 2818

Qy     124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
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Db    2819 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 2855


RESULT   9
AF002997
LOCUS       AF002997               245077 bp    DNA     linear   PRI 13-APR-2001
DEFINITION  Homo sapiens chromosome X map Xq28, complete sequence.
ACCESSION   AF002997
VERSION     AF002997.2  GI:13621226
KEYWORDS    HTG; HTGS_ACTIVEFIN.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 9444 to 72299)
  AUTHORS   Gloeckner,G., Rosenthal,A., Drescher,B., Schattevoy,R., Poustka,A.
            and Kioschis,P.
  TITLE     Genomic sequence in Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 245077)
  AUTHORS   Galgoczy,P., Schilhabel,M., Rosenthal,A. and Platzer,M.
  TITLE     Chromosome X genomic sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 245077)
  AUTHORS   Gloeckner,G., Rosenthal,A., Drescher,B. and Schattevoy,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAY-1997) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
REFERENCE   4  (bases 1 to 245077)
  AUTHORS   Platzer,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-APR-2001) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenberstr. 11, Jena, Thuringia 07745, Germany
COMMENT     On Apr 13, 2001 this sequence version replaced gi:4409798.
FEATURES             Location/Qualifiers
     source          1. .245077
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
     source          1. .211945
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="RP1-14D6"
                     /clone_lib="RPCI human PAC library 1"
     source          9444. .45606
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="LM0411, cosmid"
     source          20074. .226999
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CTD-2530F8"
                     /clone_lib="CalTech human BAC library D"
     source          33939. .72299
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="LO0630, cosmid"
     source          42555. .245077
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CTD-2507L14"
                     /clone_lib="CalTech human BAC library D"
BASE COUNT    70149 a  53336 c  52595 g  68996 t      1 others
ORIGIN


  Query Match           69.8%;  Score 157;  DB 9;  Length 245077;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-81;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 164123 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 164182

Qy      64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 164183 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 164242

Qy     124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
          |||||||||||||||||||||||||||||||||||||
Db 164243 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 164279


RESULT  10
AX019380
LOCUS       AX019380               1212 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 6 from Patent WO9940188.
ACCESSION   AX019380
VERSION     AX019380.1  GI:10043352
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1212)
  AUTHORS   Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.
  TITLE     Tumor-associated antigen derivatives from the mage family, and
            nucleic acid sequences encoding them, used for the preparation of
            fusion proteins and of compositions for vaccination
  JOURNAL   Patent: WO 9940188-A 6 12-AUG-1999;
            SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
            JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)
FEATURES             Location/Qualifiers
     source          1. .1212
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /note="Melanoma tissue"
BASE COUNT      289 a    319 c    344 g    260 t
ORIGIN


  Query Match           32.9%;  Score 74;  DB 6;  Length 1212;
  Best Local Similarity   99.2%;  Pred. No. 4.1e-32;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     708 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGTA 767
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Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
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Db     768 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 827

Qy     156 GCCCA 160
           |||||
Db     828 GCCCA 832


RESULT  11
AX019376
LOCUS       AX019376                1353 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 2 from Patent WO9940188.
ACCESSION   AX019376
VERSION     AX019376.1  GI:10043350
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1353)
  AUTHORS   Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.
  TITLE     Tumor-associated antigen derivatives from the mage family, and
            nucleic acid sequences encoding them, used for the preparation of
            fusion proteins and of compositions for vaccination
  JOURNAL   Patent: WO 9940188-A 2 12-AUG-1999;
            SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
            JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)
FEATURES             Location/Qualifiers
     source          1. .1353
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /note="Melanoma tissue"
BASE COUNT      342 a    337 c    354 g    320 t
ORIGIN


  Query Match             32.9%;  Score 74;  DB 6;  Length 1353;
  Best Local Similarity   99.2%;  Pred. No. 4.1e-32;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     849 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGTA 908

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     909 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 968

Qy     156 GCCCA 160
           |||||
Db     969 GCCCA 973


RESULT  12
AX343855
LOCUS       AX343855                1569 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 1 from Patent WO0200892.
ACCESSION   AX343855
VERSION     AX343855.1  GI:18491925
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (sites)
  AUTHORS   cabezon Silva,T.E. and Delisse,A.M.
  TITLE     Triple fusion proteins comprising ubiquitin fused between
            thioredoxin and a polypeptide of interest
  JOURNAL   Patent: WO 0200892-A 1 03-JAN-2002;
            SmithKline Beecham Biologics SA (BE)
FEATURES             Location/Qualifiers
     source          1. .1569
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Chimaeric (E. coli - human)"
BASE COUNT      391 a    400 c    433 g    345 t
ORIGIN


  Query Match             32.9%;  Score 74;  DB 6;  Length 1569;
  Best Local Similarity   99.2%;  Pred. No. 4.2e-32;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   1065 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGTA 1124

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 1184

Qy     156 GCCCA 160
           |||||
Db   1185 GCCCA 1189


RESULT  13
AR153502
LOCUS       AR153502                1640 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 11 from patent US 6235525.
ACCESSION   AR153502
VERSION     AR153502.1  GI:15121034
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1640)
  AUTHORS   van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.
  TITLE     Isolated nucleic acid molecules coding for tumor rejection antigen
            precursor MAGE-3 and uses thereof
  JOURNAL   Patent: US 6235525-A 11 22-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .1640
                     /organism="unknown"
BASE COUNT      380 a    402 c    457 g    401 t
ORIGIN


  Query Match             32.9%;  Score 74;  DB 6;  Length 1640;
  Best Local Similarity   99.2%;  Pred. No. 4.2e-32;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    639 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGTA 698

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    699 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 758

Qy     156 GCCCA 160
           |||||
Db    759 GCCCA 763


RESULT  14
I36926
LOCUS       I36926                  1640 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 11 from patent US 5612201.
ACCESSION   I36926
VERSION     I36926.1  GI:2084886
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1640)
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  AUTHORS   De Plaen,E., Boon-Falleur,T., Lethe,B., Szikora,J.-P., De Smet,C.
            and Chomez,P.
  TITLE     Isolated nucleic acid molecules useful in determining expression of
            a tumor rejection antigen precursor
  JOURNAL   Patent: US 5612201-A 11 18-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .1640
                     /organism="unknown"
BASE COUNT      380 a    402 c    457 g    401 t
ORIGIN


  Query Match             32.9%;  Score 74;  DB 6;  Length 1640;
  Best Local Similarity   99.2%;  Pred. No. 4.2e-32;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     639 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGTA 698

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     699 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 758

Qy     156 GCCCA 160
           |||||
Db     759 GCCCA 763


RESULT  15
BC011744
LOCUS       BC011744                1663 bp    mRNA    linear   PRI 02-AUG-2001
DEFINITION  Homo sapiens, Similar to melanoma antigen, family A, 3, clone
            MGC:19667 IMAGE:3345801, mRNA, complete cds.
ACCESSION   BC011744
VERSION     BC011744.1  GI:15079897
KEYWORDS    MGC.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1663)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUL-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site:       http://www.nisc.nih.gov/
            Contact:        nisc_mgc@nhgri.nih.gov
            Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
            Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
            Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
            Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 27 Row: b Column: 12
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Similarity but not
            identity to protein.
```

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FEATURES             Location/Qualifiers
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                     /tissue_type="Skin, melanotic melanoma."
                     /clone_lib="NIH_MGC_20"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     CDS             145. .1089
                     /codon_start=1
                     /product="Similar to melanoma antigen, family A, 3"
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                     /db_xref="GI:15079898"
                     /translation="MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAASSSST
                     LVEVTLGEVPAAESPDPPQSPQGASSLPTTMNYPLWSQSYEDSSNQEEEGPSTFPDLE
                     SEFQAALSRKVAELVHFLLLKYRAREPVTKAEMLGSVVGNWQYFFPVIFSKASSSLQL
                     VFGIELMEVDPIGHLYIFATCLGLSYDGLLGDNQIMPKAGLLIIVLAIIAREGDCAPE
                     EKIWEELSVLEVFEGREDSILGDPKKLLTQHFVQENYLEYRQVPGSDPACYEFLWGPR
                     ALVETSYVKVLHHMVKISGGPHISYPPLHEWVLREGEE"
BASE COUNT      411 a    398 c    448 g    406 t
ORIGIN


  Query Match             32.9%;  Score 74;  DB 9;  Length 1663;
  Best Local Similarity   99.2%;  Pred. No. 4.2e-32;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     612 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGTA 671

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     672 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 731

Qy     156 GCCCA 160
           |||||
Db     732 GCCCA 736


Search completed: May 24, 2002, 03:44:21
Job time: 7710 sec
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 02:35:01 ; Search time 246.18 Seconds
(without alignments)
1569.200 Million cell updates/sec

Title: US-08-037-230D-18
Perfect score: 225
Sequence: 1 TATTTCTTTCCTGTGATCTT.....GCGACTGTGCCCCTGAGGAG 225

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	225	100.0	225	13	AAQ32362	MAGE-6 gene. Homo
2	225	100.0	225	15	AAQ72487	Tumour rejection a
3	225	100.0	225	20	AAX84122	MAGE-6 gene. Homo
4	174	77.3	225	16	AAT01166	MAGE-6 gene. Homo
5	157	69.8	1362	20	AAX87596	CLYTA-MAGE-3-His f
6	157	69.8	1375	19	AAV22716	MAGE-6 cDNA. Homo
7	157	69.8	4204	22	AAS02056	DNA encoding molec
8	74	32.9	666	22	AAD18141	Human melanoma ass
9	74	32.9	945	22	AAD12993	Human MAGE-A3 DNA.
10	74	32.9	1212	20	AAX87592	Haemagglutinin-MAG
11	74	32.9	1353	20	AAX87588	Lipoprotein D-MAGE
12	74	32.9	1640	15	AAQ72480	Tumour rejection a
13	74	32.9	1640	20	AAX84116	MAGE-3 gene. Homo
14	74	32.9	4204	20	AAX26974	cDNA encoding MAGE
15	74	32.9	4204	21	AAA37927	Human MAGE-A3 nucl
16	74	32.9	4204	22	AAD18140	Human melanoma ass
17	69	30.7	379	18	AAT63345	Human MAGE-3 DNA.
18	69	30.7	1640	13	AAQ32355	MAGE-3 cDNA. Homo
19	56	24.9	268	18	AAT63347	Baboon MAGE-3 homo
20	56	24.9	376	18	AAT63346	Baboon MAGE-3 homo
21	49	21.8	271	18	AAT63350	Baboon MAGE-3 homo
22	49	21.8	378	18	AAT63349	Baboon MAGE-3 homo
23	43	19.1	271	18	AAT63348	Baboon MAGE-3 homo
24	36	16.0	727	22	AAD21285	Human MAGE-12 cDNA
25	36	16.0	920	22	ABA36364	Probe #14830 for g
26	36	16.0	920	22	AAI24300	Probe #14233 for g
27	36	16.0	920	22	AAI49576	Probe #18262 used
28	36	16.0	1956	22	ABA26487	Probe #4953 for ge
29	36	16.0	1956	22	AAI15118	Probe #5051 for ge
30	36	16.0	1956	22	AAI36453	Probe #5139 used t
31	36	16.0	4157	13	AAQ32353	MAGE-2 gene. Homo
32	36	16.0	4157	15	AAQ72478	Tumour rejection a
33	36	16.0	4157	20	AAX84114	MAGE-2 gene. Homo
34	27	12.0	27	15	AAQ44759	MAGE-6 nonapeptide
35	27	12.0	27	17	AAT35415	MAGE-6 nonapeptide
c 36	26	11.6	26	20	AAZ28066	MAGE-3 gene specif
37	26	11.6	1030	22	AAD21286	Human MAGE-12 gene
38	26	11.6	4523	22	AAD06131	Human MAGE-12 gene
c 39	24	10.7	24	16	AAT05065	MAGE-6 PCR primer
c 40	24	10.7	24	21	AAZ35541	Antisense PCR prim
c 41	24	10.7	24	22	AAF84241	MAGE-A6 antisense
c 42	24	10.7	24	22	AAC67098	MAGE tumour reject
43	24	10.7	27	24	ABA81874	MAGE 6 gene captur
44	24	10.7	44	18	AAV06033	cDNA encoding Mage
45	23	10.2	31	21	AAA09232	Upstream primer fo
46	23	10.2	72	22	AAD12990	Human MAGE-A1 mini
47	23	10.2	126	18	AAV06032	cDNA encoding Mage
48	23	10.2	141	24	AAI67603	ALVAC(1)-MAGE-1/3
49	23	10.2	313	24	AAI67604	ALVAC recombinant
50	23	10.2	930	22	AAD12987	Human MAGE-A1 cDNA
51	23	10.2	1084	15	AAQ67866	H6/MAGE-1 expressi
52	23	10.2	1084	20	AAZ08442	H6/MAGE-1 expressi
53	23	10.2	1094	15	AAQ67865	H6/MAGE-1 expressi
54	23	10.2	1094	20	AAZ08441	H6/MAGE-1 expressi
55	23	10.2	1338	20	AAX87593	CLYTA-MAGE-1-His f
56	23	10.2	1341	20	AAX87591	Lipoprotein D-MAGE
57	23	10.2	1624	22	AAF24676	Nucleotide sequenc
58	23	10.2	1691	20	AAV69719	Tumour rejection a
59	23	10.2	1916	21	AAA64632	cDNA encoding huma
60	23	10.2	2226	13	AAQ32360	MAGE-5 cDNA. Homo
61	23	10.2	2226	15	AAQ72485	Tumour rejection a
62	23	10.2	2226	20	AAX84104	MAGE-5 coding sequ
63	23	10.2	2305	13	AAQ32361	MAGE-51 genomic DN
64	23	10.2	2305	15	AAQ72486	Tumour rejection a
65	23	10.2	2305	16	AAT01165	MAGE-51 gene. Hom
66	23	10.2	2305	20	AAX84121	MAGE-51 gene. Hom
67	23	10.2	2418	20	AAX84103	E antigen precurso
68	23	10.2	2419	13	AAQ32351	Antigen E gene. H
69	23	10.2	2419	15	AAQ72476	Tumour rejection a
70	23	10.2	2419	16	AAT05086	MZ2-MEL antigen E
71	23	10.2	2419	20	AAX84112	Antigen E coding s
72	23	10.2	2420	15	AAQ72472	Tumour rejection a
73	23	10.2	2420	16	AAQ85435	Human melanoma ant
74	23	10.2	5674	13	AAQ32352	MAGE-1 nucleic aci
75	23	10.2	5674	15	AAQ72477	Tumour rejection a
76	23	10.2	5674	20	AAX84113	MAGE-1 gene. Homo
77	23	10.2	5724	16	AAQ98902	Tumour rejection a
78	21	9.3	27	15	AAQ44754	MAGE-3 nonapeptide
79	21	9.3	27	17	AAT35411	MAGE-3 nonapeptide
c 80	21	9.3	54	24	AAI67608	MAGE 1/3 DNA fragm
81	21	9.3	563	22	AAI43182	Probe #11868 used
82	21	9.3	1765	21	AAA64633	cDNA encoding huma

	83	21	9.3	1810	13	AAQ32364
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	86	21	9.3	1810	20	AAX84124
	87	21	9.3	1810	21	AAD01315
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	89	20	8.9	20	18	AAT63351
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	92	19	8.4	312	22	AAL16147
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c	96	19	8.4	6573	22	AAH24107
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	98	19	8.4	15071	22	AAL37613
	99	18	8.0	245	24	ABA90294
	100	18	8.0	255	24	ABA90304
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	106	18	8.0	829	22	ABA69652
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	127	17	7.6	339	22	AAS37925
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	132	17	7.6	409	22	AAI81258
	133	17	7.6	448	22	AAI93255
	134	17	7.6	451	22	AAI92728
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c	150	17	7.6	1424	24	ABA90911
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	153	17	7.6	1930	20	AAX59120
	154	17	7.6	1947	13	AAQ32363
	155	17	7.6	1947	15	AAQ72488

MAGE-8 genomic DNA
Tumour rejection a
MAGE-8 gene. Homo
MAGE-8 gene. Homo
Human MAGE-A8 part
Human MAGE-A8 gene
MAGE-3 gene forwar
Human immune/haema
Human breast cance
Human breast cance
Human breast cance
Human breast cance
Human breast cance
Human Period 1 (Pe
Human musculoskele
Human musculoskele
Human ORF101 codin
Human ORF111 codin
Human ORF28 coding
Human foetal liver
Human brain expres
Human bone marrow
Probe #9552 used t
Human foetal liver
Probe #15007 for g
Probe #15026 for g
Human foetal liver
Probe #5140 for ge
Human cDNA sequenc
Probe #5159 for ge
Human transporter
Tumour rejection a
Tumour rejection a
DNA encoding cance
DNA encoding novel
Lettuce big-vein v
DNA encoding novel
DNA encoding novel
MAGE-3 DNA fragmen
Human DNA repair a
Human secreted pro
Human secreted pro
Human breast cance
Human breast cance
Novel human diagno
Human immune/haema
Human polynucleoti
Human neuregulin g
Human neuregulin g
Human polynucleoti
Human polynucleoti
Human polynucleoti
Human secreted pro
Human cDNA clone (
Human foetal liver
Human brain expres
Human bone marrow
Probe #9975 used t
Aspergillus oryzae
Human inflammatory
DNA encoding novel
Human neuroblastom
E. coli DNA for ce
Human secreted pro
Human secreted pro
Human secreted pro
Human cDNA encodin
Human polynucleoti
Human secreted pro
Human partial ULIP
Maize UDP-glucose
MAGE-7 genomic DNA
Tumour rejection a

	156	17	7.6	1947	16	AAT01167
	157	17	7.6	1947	20	AAX84123
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	159	17	7.6	2090	21	AAC44478
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	162	17	7.6	3001	23	AAH88248
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	164	17	7.6	6759	22	AAK69181
	165	17	7.6	10159	22	AAK73470
	166	17	7.6	10159	22	AAK73471
c	167	17	7.6	10496	22	AAS41740
c	168	17	7.6	10496	22	AAK80618
c	169	17	7.6	11022	22	AAS41739
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c	173	17	7.6	20247	22	AAL36315
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c	216	16	7.1	508	22	AAK33776
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c	218	16	7.1	508	22	AAI39503
	219	16	7.1	526	21	AAZ80177
c	220	16	7.1	531	23	AAS69957
	221	16	7.1	551	23	AAS90654
c	222	16	7.1	635	21	AAZ79972
c	223	16	7.1	654	22	AAK61773
c	224	16	7.1	657	22	AAH25714
c	225	16	7.1	695	22	AAK68925
c	226	16	7.1	697	22	AAK56813
c	227	16	7.1	757	20	AAZ16318
c	228	16	7.1	802	20	AAZ16294

MAGE-7 gene. Homo
MAGE-7 gene. Homo
Capsid protein VP4
Zea mays DNA fragm
Human polynucleoti
Human polynucleoti
CNS disorder-relat
Human cDNA sequenc
Human immune/haema
Human immune/haema
Human immune/haema
Genomic sequence #
Human immune/haema
Genomic sequence #
Human immune/haema
Genomic sequence #
Human immune/haema
Human musculoskele
Human musculoskele
Propionibacterium
Human musculoskele
Human neuroblastom
Human immune/haema
Human immune/haema
Human yes1 gene.
Sequence of a synt
Human foetal liver
Probe #16546 for g
Human brain expres
Human bone marrow
Probe #15661 for g
Probe #21271 used
Human genome fragm
Human secreted exp
Human biallelic po
Human biallelic po
Human foetal liver
Human bone marrow
3' nucleotide port
Human secreted pro
Human gene express
Human single nucle
Human single nucle
DNA encoding novel
Novel human polynu
Novel human polynu
Human foetal liver
Probe #4163 for ge
Human bone marrow
Probe #4135 used t
Human foetal liver
Probe #14063 for g
Human bone marrow
Probe #9130 used t
Human foetal liver
Human renal cancer
Human bone marrow
Human foetal liver
Probe #6666 for ge
Human brain expres
Human bone marrow
Probe #6464 for ge
Probe #8189 used t
Human colon cancer
DNA encoding novel
DNA encoding novel
Human colon cancer
Human immune/haema
Human DNA polymera
Human immune/haema
Human immune/haema
Human gene express
Human gene express

c 229	16	7.1	805	22	AAI97504	Human neuroblastom
230	16	7.1	837	22	AAH31595	Human olfactory re
c 231	16	7.1	916	22	AAH99352	Human protein enco
232	16	7.1	952	22	AAH32030	Human olfactory re
233	16	7.1	961	21	AAA09237	MAGE-A4 open readi
234	16	7.1	1022	20	AAX40199	MAGE-4 encoding ge
235	16	7.1	1068	13	AAQ32359	MAGE-4 cDNA. Homo
236	16	7.1	1068	15	AAQ72484	Tumour rejection a
237	16	7.1	1068	20	AAX84120	MAGE-4 gene. Homo
238	16	7.1	1141	21	AAC47407	Arabidopsis thalia
239	16	7.1	1175	21	AAC38066	Arabidopsis thalia
c 240	16	7.1	1320	21	AAC98937	Human pancreatic c
241	16	7.1	1370	22	AAI61145	Human polynucleoti
242	16	7.1	1412	13	AAQ32365	MAGE-9 genomic DNA
243	16	7.1	1412	15	AAQ72490	Tumour rejection a
244	16	7.1	1412	16	AAT01169	MAGE-9 gene. Homo
245	16	7.1	1412	20	AAX84125	MAGE-9 gene. Homo
c 246	16	7.1	1553	24	ABA04479	Human PP712 protei
c 247	16	7.1	1603	22	AAS05992	Human DNA modifica
248	16	7.1	1612	21	AAC38992	Arabidopsis thalia
249	16	7.1	1680	22	AAF81678	Pseudomonas polyes
250	16	7.1	1680	22	AAF75376	Pseudomonas sp. st
c 251	16	7.1	1692	22	ABA09674	Human bone marrow
c 252	16	7.1	1765	21	AAA64633	cDNA encoding huma
c 253	16	7.1	1810	13	AAQ32364	MAGE-8 genomic DNA
c 254	16	7.1	1810	15	AAQ72489	Tumour rejection a
c 255	16	7.1	1810	16	AAT01168	MAGE-8 gene. Homo
c 256	16	7.1	1810	20	AAX84124	MAGE-8 gene. Homo
c 257	16	7.1	1810	21	AAD01315	Human MAGE-A8 part
258	16	7.1	1810	22	AAS30528	DNA encoding novel
259	16	7.1	1810	22	AAL06306	Human reproductive
260	16	7.1	1822	20	AAX22132	Human secreted pro
261	16	7.1	1826	20	AAV34003	Pseudomonas specie
262	16	7.1	1831	21	AAA64634	cDNA encoding huma
263	16	7.1	1834	22	AAS30527	DNA encoding novel
264	16	7.1	1834	22	AAL06305	Human reproductive
c 265	16	7.1	1872	20	AAX00622	Human secreted pro
c 266	16	7.1	2041	20	AAX22118	Human secreted pro
c 267	16	7.1	2210	23	ABL05481	Drosophila melanog
c 268	16	7.1	2281	22	AAH17057	Human cDNA sequenc
c 269	16	7.1	2306	22	AAH15696	Human cDNA sequenc
270	16	7.1	2416	22	AAH99562	Human protein enco
271	16	7.1	2531	13	AAQ32358	MAGE-41 gene. Hom
272	16	7.1	2531	13	AAQ32357	MAGE-4 gene. Homo
273	16	7.1	2531	15	AAQ72482	Tumour rejection a
274	16	7.1	2531	15	AAQ72483	Tumour rejection a
275	16	7.1	2531	20	AAX84118	MAGE-4 gene. Homo
276	16	7.1	2531	20	AAX84119	MAGE-41 gene. Hom
c 277	16	7.1	2678	22	AAH25712	Human DNA polymera
c 278	16	7.1	2679	22	AAI59359	Human polynucleoti
c 279	16	7.1	2774	15	AAQ66579	Sorbitol dehydroge
280	16	7.1	2899	23	ABL06546	Drosophila melanog
c 281	16	7.1	3048	23	AAS68823	DNA encoding novel
282	16	7.1	3788	22	AAH16109	Human cDNA sequenc
c 283	16	7.1	3839	21	AAD01314	Human MAGE-A8 gene
284	16	7.1	4206	22	AAS36384	Human cardiovascul
285	16	7.1	4272	23	ABL05480	Drosophila melanog
286	16	7.1	4368	14	AAQ49902	Glutamic acid rece
287	16	7.1	4512	24	ABI99832	Mouse ischaemic co
288	16	7.1	4790	22	AAI60062	Human polynucleoti
289	16	7.1	4808	15	AAQ79375	Human N-methyl-D-a
290	16	7.1	4808	20	AAV82892	Human N-methyl-D-a
291	16	7.1	4808	21	AAA95015	Human N-methyl-D-a
292	16	7.1	4808	21	AAZ38706	Human NMDAR2A subu
293	16	7.1	4808	24	ABI99172	Human NMDAR2A enco
294	16	7.1	4858	15	AAQ65488	Human NMDA R2A rec
c 295	16	7.1	5092	22	AAI58276	Human polynucleoti
c 296	16	7.1	5418	22	AAK53412	Human polynucleoti
c 297	16	7.1	5418	22	AAI60616	Human polynucleoti
298	16	7.1	5571	22	AAI58830	Human polynucleoti
299	16	7.1	5700	23	AAS66584	DNA encoding novel
300	16	7.1	5814	22	AAK52428	Human polynucleoti
301	16	7.1	5948	22	AAS06044	Angiotensin conver
302	16	7.1	6029	22	AAF81680	Pseudomonas polyes
303	16	7.1	6151	16	AAQ99961	Human excitatory a
304	16	7.1	6260	19	AAV52729	Human hepatocyte n
305	16	7.1	7146	19	AAV38933	Nucleic acid seque
c 306	16	7.1	8140	22	ABA20556	Human nervous syst
307	16	7.1	8165	22	AAK82672	Human immune/haema
c 308	16	7.1	8452	22	AAS59864	Human novel cytoki
309	16	7.1	8580	24	AAS96694	Arabidopsis DMT4 (
c 310	16	7.1	8734	22	ABA09012	Human TRAP240 homo
c 311	16	7.1	8734	22	AAI59594	Human polynucleoti
c 312	16	7.1	8761	22	AAI57808	Human polynucleoti
c 313	16	7.1	8785	23	AAS85661	DNA encoding novel
c 314	16	7.1	11742	22	ABA20557	Human nervous syst
315	16	7.1	11742	22	AAK76069	Human immune/haema
c 316	16	7.1	12468	22	AAK67330	Human immune/haema
317	16	7.1	13419	23	ABL06569	Drosophila melanog
c 318	16	7.1	14040	22	ABA08209	Human ovarian and
c 319	16	7.1	14040	22	AAL02790	Human reproductive
c 320	16	7.1	14040	22	AAL07517	Human reproductive
c 321	16	7.1	19401	23	ABL06568	Drosophila melanog
322	16	7.1	19596	22	AAK73967	Human immune/haema
323	16	7.1	19596	22	AAK73968	Human immune/haema
324	16	7.1	25002	19	AAV52181	Streptococcus pneu
c 325	16	7.1	26591	22	AAL36313	Human musculoskele
326	16	7.1	26995	22	AAS29963	Human lung antigen
c 327	16	7.1	29163	22	AAL05121	Human reproductive
c 328	16	7.1	31969	23	ABL07768	Drosophila melanog
c 329	15	6.7	21	21	AAZ59313	Human STP2 gene pr
c 330	15	6.7	51	22	AAI77770	Human silent SNP c
c 331	15	6.7	51	22	AAI77771	Human silent SNP c
c 332	15	6.7	51	22	AAI77772	Human silent SNP c
c 333	15	6.7	51	22	AAI77773	Human silent SNP c
c 334	15	6.7	57	21	AAZ89633	HIV-2 ROD isolate
335	15	6.7	118	22	AAL26303	Human breast cance
336	15	6.7	121	20	AAH86391	Human single nucle
337	15	6.7	129	19	AAV41900	Nucleotide sequenc
338	15	6.7	138	19	AAV41893	Nucleotide sequenc
339	15	6.7	138	22	AAA89244	Chicken growth hor
340	15	6.7	139	22	ABA74725	Human foetal liver
341	15	6.7	139	22	ABA39436	Probe #17902 for g
342	15	6.7	139	22	AAK49384	Human bone marrow
343	15	6.7	139	22	AAI26495	Probe #16428 for g
344	15	6.7	272	21	AAC02812	Human secreted pro
c 345	15	6.7	292	22	ABA71283	Human foetal liver
c 346	15	6.7	292	22	AAK19585	Human brain expres
c 347	15	6.7	292	22	AAK45588	Human bone marrow
c 348	15	6.7	292	22	AAI51524	Probe #20210 used
349	15	6.7	303	22	ABA16778	Human nervous syst
350	15	6.7	306	22	AAI09757	Probe #9748 used t
351	15	6.7	311	22	ABA12049	Human nervous syst
352	15	6.7	324	21	AAC29237	Human secreted pro
353	15	6.7	328	21	AAC56647	Eucalyptus grandis
c 354	15	6.7	345	22	AAS37860	Novel human diagno
355	15	6.7	346	22	AAI88734	Human polynucleoti
356	15	6.7	362	22	ABA08365	Human PLA2 homolog
357	15	6.7	374	22	AAI86606	Human polynucleoti
c 358	15	6.7	383	22	AAI98945	Human excretory re
c 359	15	6.7	383	22	AAI63295	Human kidney relat
360	15	6.7	389	20	AAX01140	M. tuberculosis an
361	15	6.7	389	20	AAX01174	M. tuberculosis an
362	15	6.7	389	22	AAS12484	Mycobacterium tube
363	15	6.7	391	21	AAC05312	Human secreted pro
364	15	6.7	393	21	AAC76133	Human ORFX ORF1688
365	15	6.7	402	22	AAF67166	Novel human polynu
366	15	6.7	414	22	AAL19253	Human breast cance
367	15	6.7	429	22	AAL08558	Human breast cance
368	15	6.7	435	22	AAI04773	Probe #4764 used t
369	15	6.7	445	22	ABA43372	Human breast cell
370	15	6.7	445	22	ABA53815	Human foetal liver
371	15	6.7	445	22	ABA23564	Probe #2030 for ge
372	15	6.7	445	22	AAK02077	Human brain expres
373	15	6.7	445	22	AAI12110	Probe #2043 for ge
374	15	6.7	445	22	AAI33451	Probe #2137 used t

	375	15	6.7	445	22	AAI02031	Probe #2022 used t
	376	15	6.7	459	21	AAC38179	Arabidopsis thalia
	377	15	6.7	462	22	AAD08333	Human secreted pro
c	378	15	6.7	466	22	ABA58624	Human foetal liver
c	379	15	6.7	466	22	AAK06751	Human brain expres
c	380	15	6.7	466	22	AAK32462	Human bone marrow
c	381	15	6.7	466	22	AAI38296	Probe #6982 used t
	382	15	6.7	470	21	AAC57215	Eucalyptus grandis
	383	15	6.7	508	22	AAL01474	Human reproductive
	384	15	6.7	510	22	AAL05246	Human reproductive
	385	15	6.7	513	22	AAH35349	Human colon cancer
c	386	15	6.7	536	22	AAK62873	Human immune/haema
	387	15	6.7	541	23	ABL11369	Drosophila melanog
c	388	15	6.7	543	22	AAH09833	Human cDNA clone (
c	389	15	6.7	543	22	AAH09896	Human cDNA clone (
	390	15	6.7	556	22	AAS26770	Human genomic DNA
c	391	15	6.7	558	23	AAS91397	DNA encoding novel
c	392	15	6.7	571	22	AAK92505	Human cDNA 3'-end
	393	15	6.7	595	22	ABA63027	Human foetal liver
	394	15	6.7	595	22	ABA30287	Probe #8753 for ge
	395	15	6.7	595	22	AAK37229	Human bone marrow
	396	15	6.7	595	22	AAI18060	Probe #7993 for ge
	397	15	6.7	612	22	AAK91931	Human cDNA 5'-end
	398	15	6.7	612	22	AAK93341	Human cDNA clone r
	399	15	6.7	637	22	AAI63864	Human polynucleoti
c	400	15	6.7	650	23	AAS77780	DNA encoding novel
	401	15	6.7	687	21	AAC03777	Human secreted pro
c	402	15	6.7	696	23	AAS64851	DNA encoding novel
	403	15	6.7	701	22	AAK66401	Human immune/haema
c	404	15	6.7	735	21	AAC49868	Arabidopsis thalia
	405	15	6.7	736	22	AAI97143	Human neuroblastom
	406	15	6.7	744	23	AAS67339	DNA encoding novel
	407	15	6.7	745	22	AAS32894	Human genomic DNA
	408	15	6.7	745	22	AAS32895	Human genomic DNA
c	409	15	6.7	766	21	AAZ97266	Human prostate can
c	410	15	6.7	767	23	ABL19951	Drosophila melanog
c	411	15	6.7	774	22	AAL22106	Human breast cance
	412	15	6.7	780	22	AAS31394	Human cDNA encodin
c	413	15	6.7	811	21	AAC49886	Arabidopsis thalia
c	414	15	6.7	812	21	AAC40364	Arabidopsis thalia
c	415	15	6.7	838	22	AAK66649	Human immune/haema
c	416	15	6.7	838	22	AAK71928	Human immune/haema
	417	15	6.7	850	22	AAH05401	Human cDNA clone (
c	418	15	6.7	854	21	AAD00290	Rice histidine bio
	419	15	6.7	887	22	AAH31614	Human olfactory re
	420	15	6.7	890	22	AAL21953	Human breast cance
c	421	15	6.7	903	21	AAZ61638	cDNA encoding muri
c	422	15	6.7	903	22	AAC99571	Skin cell cDNA, SE
	423	15	6.7	908	22	AAL24826	Human breast cance
	424	15	6.7	920	13	AAQ32366	MAGE-10 genomic DN
	425	15	6.7	920	15	AAQ72491	Tumour rejection a
	426	15	6.7	920	16	AAT01170	MAGE-10 gene. Hom
	427	15	6.7	920	20	AAX84126	MAGE-10 gene. Hom
	428	15	6.7	920	21	AAD01313	Human MAGE-A10 par
	429	15	6.7	935	22	AAI66460	Human ankyrin 27 c
	430	15	6.7	957	22	AAH31653	Human olfactory re
	431	15	6.7	960	22	AAH32344	Human olfactory re
c	432	15	6.7	976	22	AAK42326	Human bone marrow
c	433	15	6.7	976	22	AAI23105	Probe #13038 for g
c	434	15	6.7	976	22	AAI48408	Probe #17094 used
c	435	15	6.7	976	22	AAI08754	Probe #8745 used t
	436	15	6.7	978	22	AAH31933	Human olfactory re
	437	15	6.7	997	22	AAD08303	Human secreted pro
c	438	15	6.7	1024	21	AAZ97161	Human prostate can
c	439	15	6.7	1024	21	AAZ97165	Human prostate can
c	440	15	6.7	1024	21	AAZ97225	Human prostate can
	441	15	6.7	1044	22	AAS42286	Human cDNA encodin
	442	15	6.7	1066	22	AAD04777	Human death domain
	443	15	6.7	1077	21	AAA55224	C. symbiosum open
	444	15	6.7	1079	19	AAV41891	Alternatively spli
	445	15	6.7	1088	19	AAV41890	Nucleotide sequenc
c	446	15	6.7	1140	19	AAV71081	Alpha-actinin acti
	447	15	6.7	1174	20	AAX87944	Human G protein co
c	448	15	6.7	1242	23	ABL21917	Drosophila melanog
c	449	15	6.7	1266	22	AAH67260	C glutamicum codin
c	450	15	6.7	1276	22	AAS12520	Gene #13 encoding
	451	15	6.7	1279	21	AAZ51790	Wheat farnesyltran
	452	15	6.7	1287	22	AAI63858	Human polynucleoti
	453	15	6.7	1294	22	AAI59556	Human polynucleoti
	454	15	6.7	1309	22	AAL01520	Human reproductive
	455	15	6.7	1309	22	AAI63939	Human polynucleoti
c	456	15	6.7	1311	20	AAX33189	Human origin of re
c	457	15	6.7	1311	21	AAZ61769	cDNA encoding mous
c	458	15	6.7	1311	22	AAC99702	Skin cell cDNA, SE
	459	15	6.7	1319	22	AAS33310	DNA encoding human
c	460	15	6.7	1323	23	ABL07519	Drosophila melanog
c	461	15	6.7	1338	22	AAI99982	Human FVII encodin
c	462	15	6.7	1357	22	AAI99983	Human FVII express
c	463	15	6.7	1368	22	AAF71126	C. glutamicum SRT
c	464	15	6.7	1370	21	AAA26413	Human secreted pro
	465	15	6.7	1386	23	AAS91398	DNA encoding novel
	466	15	6.7	1401	22	AAH62715	Shrimp white spot
c	467	15	6.7	1405	21	AAC38496	Arabidopsis thalia
c	468	15	6.7	1408	21	AAC47679	Arabidopsis thalia
	469	15	6.7	1461	21	AAA15960	Human protein clon
c	470	15	6.7	1463	22	AAS23104	DNA encoding novel
	471	15	6.7	1506	24	AAS62337	cDNA sequence #124
	472	15	6.7	1510	21	AAF15123	Trichoderma reesei
	473	15	6.7	1516	22	AAH16017	Human cDNA sequenc
	474	15	6.7	1534	23	AAS72018	DNA encoding novel
	475	15	6.7	1536	22	AAH76663	Human cell growth
	476	15	6.7	1541	21	AAC55202	Human secreted pro
	477	15	6.7	1545	22	AAF72765	Human prostate can
c	478	15	6.7	1566	23	ABL03693	Drosophila melanog
	479	15	6.7	1570	21	AAC76369	Human ORFX ORF1924
c	480	15	6.7	1588	21	AAC51278	Arabidopsis thalia
c	481	15	6.7	1592	21	AAC40157	Arabidopsis thalia
	482	15	6.7	1636	15	AAQ58006	Sequence of plasmi
	483	15	6.7	1660	22	AAS27772	DNA encoding novel
c	484	15	6.7	1667	22	AAK94481	Human full-length
	485	15	6.7	1668	23	AAS73598	DNA encoding novel
	486	15	6.7	1668	23	AAS79823	DNA encoding novel
	487	15	6.7	1671	22	AAF33038	Human secreted pro
	488	15	6.7	1691	21	AAF12937	Aspergillus oryzae
	489	15	6.7	1723	22	AAS03054	Human diagnostic a
	490	15	6.7	1736	22	AAH15523	Human cDNA sequenc
c	491	15	6.7	1756	23	ABL13919	Drosophila melanog
	492	15	6.7	1836	24	ABI99435	Mouse ischaemic co
c	493	15	6.7	1862	21	AAC48614	Arabidopsis thalia
c	494	15	6.7	1864	21	AAC40212	Arabidopsis thalia
	495	15	6.7	1871	13	AAQ26959	Guinea pig PAF rec
c	496	15	6.7	1883	23	AAS69005	DNA encoding novel
	497	15	6.7	1902	22	AAK94664	Human full-length
	498	15	6.7	1914	23	ABL27825	Drosophila melanog
c	499	15	6.7	1932	22	AAI67196	Nucleotide sequenc
c	500	15	6.7	1956	22	AAK29286	Human bone marrow
c	501	15	6.7	1956	22	AAI13887	Probe #3820 for ge
c	502	15	6.7	1956	22	AAI35249	Probe #3935 used t
c	503	15	6.7	1956	22	AAI03750	Probe #3741 used t
c	504	15	6.7	1962	22	AAI67197	Nucleotide sequenc
	505	15	6.7	1964	23	AAS84606	DNA encoding novel
	506	15	6.7	2029	22	AAH15472	Human cDNA sequenc
c	507	15	6.7	2045	22	AAK51985	Human polynucleoti
	508	15	6.7	2057	22	AAH14091	Human cDNA sequenc
	509	15	6.7	2086	24	ABA05349	Human initiation f
	510	15	6.7	2152	22	AAS33119	DNA encoding human
	511	15	6.7	2156	20	AAZ10807	Polynucleotide seq
	512	15	6.7	2156	22	AAS59263	Human cDNA encodin
	513	15	6.7	2156	24	ABA90932	Human polynucleoti
	514	15	6.7	2168	21	AAA15970	Human protein clon
c	515	15	6.7	2181	23	ABL27979	Drosophila melanog
c	516	15	6.7	2199	21	AAC69538	Human secreted pro
	517	15	6.7	2209	24	AAS62822	cDNA sequence #609
	518	15	6.7	2294	22	AAD08300	Human secreted pro
	519	15	6.7	2372	22	AAF93908	Human cDNA encodin
	520	15	6.7	2427	15	AAQ70435	Human glyco-protei

	521	15	6.7	2474	23	ABL15009	Drosophila melanog
c	522	15	6.7	2488	22	AAH17612	Human cDNA sequenc
c	523	15	6.7	2541	23	ABL11368	Drosophila melanog
	524	15	6.7	2548	23	ABL27826	Drosophila melanog
	525	15	6.7	2559	19	AAV26618	MAGE-10 tumour rej
	526	15	6.7	2559	21	AAD01312	Human MAGE-A10 cDN
	527	15	6.7	2559	21	AAA52965	Human tumour rejec
	528	15	6.7	2560	21	AAA75111	cDNA encoding a hu
	529	15	6.7	2603	22	AAH13930	Human cDNA sequenc
c	530	15	6.7	2610	24	AAS96324	Arabidopsis cDNA e
c	531	15	6.7	2673	9	AAN82199	ENVRN sequence fro
	532	15	6.7	2688	23	ABL07343	Drosophila melanog
	533	15	6.7	2742	23	AAS51581	Pseudomonas aerugi
	534	15	6.7	2757	22	AAS26875	Human cDNA encodin
c	535	15	6.7	2757	23	ABL23365	Drosophila melanog
	536	15	6.7	2812	22	AAK78486	Human immune/haema
	537	15	6.7	2856	23	ABL22267	Drosophila melanog
	538	15	6.7	2895	22	AAF32642	Human cDNA encodin
c	539	15	6.7	2903	23	AAS78152	DNA encoding novel
c	540	15	6.7	2919	21	AAZ90526	Human GPCR protein
c	541	15	6.7	2929	21	AAZ52366	NSEQ gene-18 assoc
c	542	15	6.7	2973	22	AAH17771	Human cDNA sequenc
	543	15	6.7	2997	22	AAK94769	Human full-length
c	544	15	6.7	3000	21	AAZ87930	Human brain-derive
c	545	15	6.7	3001	23	AAH88249	CNS disorder-relat
	546	15	6.7	3015	23	ABL04274	Drosophila melanog
	547	15	6.7	3072	21	AAF16331	Human prostate can
c	548	15	6.7	3081	22	ABA82677	Alpha-actinin (ACT
	549	15	6.7	3092	21	AAF18291	Lung cancer associ
	550	15	6.7	3095	22	AAK82207	Human immune/haema
	551	15	6.7	3127	23	ABL03828	Drosophila melanog
	552	15	6.7	3143	22	AAI61342	Human polynucleoti
c	553	15	6.7	3144	23	ABL19950	Drosophila melanog
c	554	15	6.7	3334	22	AAK82796	Human immune/haema
	555	15	6.7	3399	21	AAC99113	Human pancreatic c
	556	15	6.7	3447	23	ABL16117	Drosophila melanog
c	557	15	6.7	3472	23	AAS72696	DNA encoding novel
c	558	15	6.7	3504	22	AAH15784	Human cDNA sequenc
	559	15	6.7	3510	21	AAD01311	Human MAGE-A10 gen
c	560	15	6.7	3543	23	ABL07543	Drosophila melanog
	561	15	6.7	3561	23	AAS76613	DNA encoding novel
	562	15	6.7	3566	23	ABL07518	Drosophila melanog
	563	15	6.7	3689	22	ABA83088	DKFZp5860031 ovari
c	564	15	6.7	3707	22	AAF80532	Receptor #20 parti
	565	15	6.7	3736	22	AAK85055	Human immune/haema
c	566	15	6.7	3762	22	AAK76204	Human immune/haema
	567	15	6.7	3825	22	AAS01561	Human secretory mo
	568	15	6.7	3914	23	ABL27824	Drosophila melanog
c	569	15	6.7	3923	23	ABL21916	Drosophila melanog
c	570	15	6.7	3950	20	AAZ34259	Human PRO768 nucle
c	571	15	6.7	3951	21	AAC78566	Human PRO768 (UNQ4
c	572	15	6.7	3951	22	AAS45984	Human DNA encoding
	573	15	6.7	3977	24	ABL01591	Human secreted pro
	574	15	6.7	3989	20	AAV84428	Human secreted pro
	575	15	6.7	3989	22	ABA83211	Human secreted pro
	576	15	6.7	4024	23	ABL05958	Drosophila melanog
	577	15	6.7	4033	22	AAF90327	Human JAFFA genomi
	578	15	6.7	4042	22	AAK51596	Human polynucleoti
c	579	15	6.7	4080	22	AAC83438	Human integrin alp
	580	15	6.7	4102	22	AAS01489	Human secreted pro
	581	15	6.7	4181	23	ABL21702	Drosophila melanog
c	582	15	6.7	4204	21	AAC81925	Vector pCM-ENV(ROD
c	583	15	6.7	4204	21	AAC81939	Envelope vector pC
c	584	15	6.7	4276	23	ABL17383	Drosophila melanog
c	585	15	6.7	4300	23	ABL17307	Drosophila melanog
c	586	15	6.7	4310	19	AAV34856	Drosophila melanog
	587	15	6.7	4340	23	ABL13918	Drosophila melanog
	588	15	6.7	4350	22	AAD09490	Human immunodefici
	589	15	6.7	4375	22	AAS63188	Human purified sec
	590	15	6.7	4382	22	AAS44669	Human full-length
	591	15	6.7	4406	23	ABL03692	Drosophila melanog
c	592	15	6.7	4443	22	AAH57448	Human lung cell sp
	593	15	6.7	4487	23	ABL15982	Drosophila melanog
	594	15	6.7	4499	22	AAI58788	Human polynucleoti
	595	15	6.7	4499	22	AAI58789	Human polynucleoti
	596	15	6.7	4586	22	AAI60573	Human polynucleoti
	597	15	6.7	4586	22	AAI60574	Human polynucleoti
	598	15	6.7	4586	22	AAI60575	Human polynucleoti
	599	15	6.7	4616	22	AAH98704	Human EST-derived
	600	15	6.7	4636	19	AAV23920	Human alpha3 integ
c	601	15	6.7	4681	23	ABL15008	Drosophila melanog
	602	15	6.7	4702	23	ABL09844	Drosophila melanog
	603	15	6.7	4724	22	AAI58787	Human polynucleoti
	604	15	6.7	4825	23	ABL07342	Drosophila melanog
	605	15	6.7	4867	23	ABL07564	Drosophila melanog
	606	15	6.7	4886	21	AAC76173	Human ORFX ORF1728
	607	15	6.7	4907	22	AAF26592	DNA encoding human
c	608	15	6.7	5176	19	AAV04017	Human multiple mye
	609	15	6.7	5456	22	AAK52580	Human polynucleoti
	610	15	6.7	5499	22	AAK67617	Human immune/haema
c	611	15	6.7	5672	23	ABL13120	Drosophila melanog
c	612	15	6.7	5714	22	AAS08649	Human cDNA encodin
c	613	15	6.7	5714	22	AAS08659	Human cDNA encodin
c	614	15	6.7	5726	22	AAH98377	Human EST-derived
c	615	15	6.7	5773	22	AAS08648	Human cDNA encodin
	616	15	6.7	5805	23	ABL22266	Drosophila melanog
	617	15	6.7	6096	22	AAS26766	Human genomic DNA
	618	15	6.7	6197	22	AAK85057	Human immune/haema
	619	15	6.7	6198	22	AAK85054	Human immune/haema
	620	15	6.7	6200	22	AAK85058	Human immune/haema
	621	15	6.7	6201	22	AAK85056	Human immune/haema
	622	15	6.7	6234	20	AAX20522	Polynucleotide seq
	623	15	6.7	6240	23	ABL07542	Drosophila melanog
c	624	15	6.7	6313	23	ABL23364	Drosophila melanog
c	625	15	6.7	6449	23	ABL14133	Drosophila melanog
	626	15	6.7	6454	22	AAI57932	Human polynucleoti
	627	15	6.7	6502	22	AAF98718	Human late stage o
	628	15	6.7	6529	19	AAV41889	Nucleotide sequenc
	629	15	6.7	6610	23	ABL16116	Drosophila melanog
	630	15	6.7	6645	17	AAT65002	Mouse cell cycle r
	631	15	6.7	6742	22	AAI59718	Human polynucleoti
c	632	15	6.7	7156	22	AAK86021	Human immune/haema
c	633	15	6.7	7156	22	AAK86022	Human immune/haema
	634	15	6.7	7319	24	AAS94894	Human DNA sequence
	635	15	6.7	7640	22	AAK91239	Human digestive sy
c	636	15	6.7	7961	23	ABL27070	Drosophila melanog
c	637	15	6.7	7964	23	ABL19500	Drosophila melanog
	638	15	6.7	7971	22	AAK74473	Human immune/haema
c	639	15	6.7	8174	12	AAQ13332	GDP-Fuc:beta-D-gal
c	640	15	6.7	8174	15	AAQ56908	DNA encoding a gly
c	641	15	6.7	8174	18	AAT61677	Human alpha(1,2)-f
c	642	15	6.7	8396	21	AAZ59353	Human STP2 (phenol
	643	15	6.7	8764	22	AAK91240	Human digestive sy
	644	15	6.7	9149	23	ABL14132	Drosophila melanog
c	645	15	6.7	9473	10	AAN92768	HIV-2 variant HIV-
c	646	15	6.7	9630	21	AAZ89628	HIV-2 ROD DNA. Hu
c	647	15	6.7	9643	9	AAN80859	Sequence of entire
c	648	15	6.7	9663	21	AAC81938	Packaging vector p
c	649	15	6.7	9672	13	AAQ20616	ROD HIV-2 isolate
c	650	15	6.7	9726	21	AAC81937	Packaging vector p
	651	15	6.7	9931	23	ABL17306	Drosophila melanog
c	652	15	6.7	10163	18	AAT61085	Full-length HIV-2K
	653	15	6.7	10290	23	ABL27978	Drosophila melanog
	654	15	6.7	10577	22	AAK72646	Human immune/haema
c	655	15	6.7	11136	23	ABL16298	Drosophila melanog
c	656	15	6.7	11869	22	AAS36792	Human cardiovascul
c	657	15	6.7	11987	22	AAL07284	Human reproductive
c	658	15	6.7	12112	22	AAK83784	Human immune/haema
	659	15	6.7	12259	22	AAS36190	Human cardiovascul
c	660	15	6.7	12807	22	AAL05769	Human reproductive
c	661	15	6.7	14333	22	AAK79846	Human immune/haema
	662	15	6.7	14825	23	ABL17382	Drosophila melanog
c	663	15	6.7	14918	22	AAS26792	Human genomic DNA
c	664	15	6.7	16983	22	AAK85126	Human immune/haema
	665	15	6.7	17464	23	ABL03994	Drosophila melanog
c	666	15	6.7	18974	21	AAA81485	N. meningitidis pa

c	667	15	6.7	20072	20	AAX13026	Enterococcus faeca
	668	15	6.7	21313	22	AAK82710	Human immune/haema
	669	15	6.7	22465	22	AAK86932	Human immune/haema
	670	15	6.7	22585	22	AAL04299	Human reproductive
	671	15	6.7	26225	22	AAS35776	Human cardiovascul
c	672	15	6.7	32998	21	AAA55186	Cenarchaeum symbio
	673	15	6.7	33780	22	AAH24652	Nucleotide sequenc
c	674	15	6.7	35829	23	AAS59573	Propionibacterium
	675	15	6.7	36519	19	AAV22141	Chimpanzee adenovi
c	676	15	6.7	38059	22	AAF54018	Human factor IX (h
	677	15	6.7	42979	23	ABL20870	Drosophila melanog
c	678	15	6.7	45265	21	AAZ46508	Sequence of a COSM
	679	15	6.7	49999	20	AAZ23903	Human LOBO homolog
	680	15	6.7	50000	20	AAX23517	Human kidney amino
c	681	15	6.7	56583	21	AAF21125	Human low adenosin
c	682	15	6.7	56583	21	AAA35003	Human adenosine re
c	683	15	6.7	61313	23	AAS59545	Propionibacterium
c	684	15	6.7	72049	22	ABA82623	Human HBM gene reg
	685	15	6.7	74962	22	AAD15256	Human phosphatase
	686	15	6.7	125910	21	AAC64370	Human KCNQ5 (KCN6q
	687	15	6.7	305107	22	AAH62689	Shrimp white spot
	688	15	6.7	349980	21	AAF21607	Neisseria meningit
	689	15	6.7	349980	22	AAH68531	C glutamicum codin
c	690	15	6.7	1230025	20	AAX91990	Nucleotide sequenc
	691	15	6.7	1437668	21	AAA81490	N. meningitidis B
	692	14	6.2	18	22	AAF81317	Human cacng8 PCR p
	693	14	6.2	20	21	AAC80118	Reverse primer #30
c	694	14	6.2	20	22	AAD06140	Human MAGE-A12 gen
	695	14	6.2	20	24	ABI97419	Capture oligonucle
	696	14	6.2	21	21	AAC80113	Reverse primer #25
	697	14	6.2	21	21	AAC80119	Reverse primer #31
	698	14	6.2	21	21	AAA36933	Human dysferlin ex
	699	14	6.2	21	21	AAA11478	Human dysferlin PC
	700	14	6.2	22	21	AAC80114	Reverse primer #26
	701	14	6.2	22	21	AAC80120	Reverse primer #32
	702	14	6.2	23	21	AAC80115	Reverse primer #27
	703	14	6.2	23	21	AAC80121	Reverse primer #33
	704	14	6.2	24	21	AAC80116	Reverse primer #28
	705	14	6.2	24	21	AAC80122	Reverse primer #34
	706	14	6.2	24	24	ABI91408	Capture oligonucle
c	707	14	6.2	24	24	ABI91409	Capture oligonucle
	708	14	6.2	25	21	AAC80117	Reverse primer #29
	709	14	6.2	25	21	AAC80123	Reverse primer #35
c	710	14	6.2	38	21	AAA11526	Drosophila sp. TGF
	711	14	6.2	49	24	AAI67605	MAGE-1 DNA fragmen
	712	14	6.2	50	13	AAQ28134	Human T lymphocyte
	713	14	6.2	81	16	AAT04790	TCR CDR3 V-alpha r
	714	14	6.2	122	18	AAV02805	Human RHAMM genomi
c	715	14	6.2	130	22	ABA11561	Human nervous syst
	716	14	6.2	144	22	AAK15314	Human brain expres
	717	14	6.2	144	22	AAK41035	Human bone marrow
c	718	14	6.2	158	16	AAT20252	Human gene signatu
	719	14	6.2	158	21	AAC15608	Human secreted pro
c	720	14	6.2	165	16	AAQ98921	TGF-beta inducible
c	721	14	6.2	177	19	AAX10468	Human biallelic po
c	722	14	6.2	177	20	AAX18098	Coding sequence fo
	723	14	6.2	181	22	AAS63961	Human prostate cDN
	724	14	6.2	181	22	AAS63962	Human prostate cDN
c	725	14	6.2	211	21	AAC10642	Human secreted pro
c	726	14	6.2	219	19	AAX11713	Human biallelic po
c	727	14	6.2	219	19	AAX12878	Human biallelic po
	728	14	6.2	223	16	AAT01041	Mouse B7-2 exon m1
	729	14	6.2	231	21	AAZ80203	Human colon cancer
c	730	14	6.2	235	20	AAX37976	Histocompatibility
c	731	14	6.2	240	19	AAV46152	Human HLA-A intron
c	732	14	6.2	240	21	AAC80402	HLA-A intron 2 seq
c	733	14	6.2	240	21	AAC80407	HLA-A intron 2 seq
c	734	14	6.2	240	21	AAC80408	HLA-A intron 2 seq
c	735	14	6.2	240	21	AAC80409	HLA-A intron 2 seq
c	736	14	6.2	240	21	AAC80410	HLA-A intron 2 seq
c	737	14	6.2	241	19	AAV46142	Human HLA-A intron
c	738	14	6.2	241	19	AAV46143	Human HLA-A intron
c	739	14	6.2	241	19	AAV46144	Human HLA-A intron
c	740	14	6.2	241	19	AAV46145	Human HLA-A intron
c	741	14	6.2	241	19	AAV46146	Human HLA-A intron
c	742	14	6.2	241	19	AAV46147	Human HLA-A intron
c	743	14	6.2	241	19	AAV46148	Human HLA-A intron
c	744	14	6.2	241	19	AAV46149	Human HLA-A intron
c	745	14	6.2	241	19	AAV46150	Human HLA-A intron
c	746	14	6.2	241	19	AAV46151	Human HLA-A intron
c	747	14	6.2	241	19	AAV46132	Human HLA-A intron
c	748	14	6.2	241	19	AAV46133	Human HLA-A intron
c	749	14	6.2	241	19	AAV46134	Human HLA-A intron
c	750	14	6.2	241	19	AAV46135	Human HLA-A intron
c	751	14	6.2	241	19	AAV46136	Human HLA-A intron
c	752	14	6.2	241	19	AAV46137	Human HLA-A intron
c	753	14	6.2	241	19	AAV46138	Human HLA-A intron
c	754	14	6.2	241	19	AAV46139	Human HLA-A intron
c	755	14	6.2	241	19	AAV46140	Human HLA-A intron
c	756	14	6.2	241	19	AAV46141	Human HLA-A intron
c	757	14	6.2	241	19	AAV46131	Human HLA-A intron
c	758	14	6.2	241	19	AAV46117	Human HLA-A intron
c	759	14	6.2	241	19	AAV46118	Human HLA-A intron
c	760	14	6.2	241	19	AAV46119	Human HLA-A intron
c	761	14	6.2	241	19	AAV46120	Human HLA-A intron
c	762	14	6.2	241	19	AAV46121	Human HLA-A intron
c	763	14	6.2	241	19	AAV46122	Human HLA-A intron
c	764	14	6.2	241	19	AAV46123	Human HLA-A intron
c	765	14	6.2	241	19	AAV46124	Human HLA-A intron
c	766	14	6.2	241	19	AAV46125	Human HLA-A intron
c	767	14	6.2	241	19	AAV46126	Human HLA-A intron
c	768	14	6.2	241	19	AAV46127	Human HLA-A intron
c	769	14	6.2	241	19	AAV46128	Human HLA-A intron
c	770	14	6.2	241	19	AAV46129	Human HLA-A intron
c	771	14	6.2	241	19	AAV46130	Human HLA-A intron
c	772	14	6.2	241	19	AAV46106	Human HLA-A intron
c	773	14	6.2	241	19	AAV46107	Human HLA-A intron
c	774	14	6.2	241	19	AAV46108	Human HLA-A intron
c	775	14	6.2	241	19	AAV46109	Human HLA-A intron
c	776	14	6.2	241	19	AAV46110	Human HLA-A intron
c	777	14	6.2	241	19	AAV46111	Human HLA-A intron
c	778	14	6.2	241	19	AAV46112	Human HLA-A intron
c	779	14	6.2	241	19	AAV46113	Human HLA-A intron
c	780	14	6.2	241	19	AAV46114	Human HLA-A intron
c	781	14	6.2	241	19	AAV46115	Human HLA-A intron
c	782	14	6.2	241	19	AAV46116	Human HLA-A intron
c	783	14	6.2	241	20	AAX37968	Histocompatibility
c	784	14	6.2	241	20	AAX37969	Histocompatibility
c	785	14	6.2	241	20	AAX37970	Histocompatibility
c	786	14	6.2	241	20	AAX37971	Histocompatibility
c	787	14	6.2	241	20	AAX37972	Histocompatibility
c	788	14	6.2	241	20	AAX37973	Histocompatibility
c	789	14	6.2	241	20	AAX37974	Histocompatibility
c	790	14	6.2	241	20	AAX37975	Histocompatibility
c	791	14	6.2	241	20	AAX37977	Histocompatibility
c	792	14	6.2	241	20	AAX37952	Histocompatibility
c	793	14	6.2	241	20	AAX37953	Histocompatibility
c	794	14	6.2	241	20	AAX37954	Histocompatibility
c	795	14	6.2	241	20	AAX37955	Histocompatibility
c	796	14	6.2	241	20	AAX37956	Histocompatibility
c	797	14	6.2	241	20	AAX37957	Histocompatibility
c	798	14	6.2	241	20	AAX37958	Histocompatibility
c	799	14	6.2	241	20	AAX37959	Histocompatibility
c	800	14	6.2	241	20	AAX37960	Histocompatibility
c	801	14	6.2	241	20	AAX37961	Histocompatibility
c	802	14	6.2	241	20	AAX37962	Histocompatibility
c	803	14	6.2	241	20	AAX37963	Histocompatibility
c	804	14	6.2	241	20	AAX37964	Histocompatibility
c	805	14	6.2	241	20	AAX37965	Histocompatibility
c	806	14	6.2	241	20	AAX37966	Histocompatibility
c	807	14	6.2	241	20	AAX37967	Histocompatibility
c	808	14	6.2	241	20	AAX37936	Histocompatibility
c	809	14	6.2	241	20	AAX37937	Histocompatibility
c	810	14	6.2	241	20	AAX37938	Histocompatibility
c	811	14	6.2	241	20	AAX37939	Histocompatibility
c	812	14	6.2	241	20	AAX37940	Histocompatibility

c 813	14	6.2	241	20	AAX37941	Histocompatibility
c 814	14	6.2	241	20	AAX37942	Histocompatibility
c 815	14	6.2	241	20	AAX37943	Histocompatibility
c 816	14	6.2	241	20	AAX37944	Histocompatibility
c 817	14	6.2	241	20	AAX37945	Histocompatibility
c 818	14	6.2	241	20	AAX37946	Histocompatibility
c 819	14	6.2	241	20	AAX37947	Histocompatibility
c 820	14	6.2	241	20	AAX37948	Histocompatibility
c 821	14	6.2	241	20	AAX37949	Histocompatibility
c 822	14	6.2	241	20	AAX37950	Histocompatibility
c 823	14	6.2	241	20	AAX37951	Histocompatibility
c 824	14	6.2	241	20	AAX37931	Histocompatibility
c 825	14	6.2	241	20	AAX37932	Histocompatibility
c 826	14	6.2	241	20	AAX37933	Histocompatibility
c 827	14	6.2	241	20	AAX37934	Histocompatibility
c 828	14	6.2	241	20	AAX37935	Histocompatibility
c 829	14	6.2	241	21	AAC80396	HLA-A intron 2 seq
c 830	14	6.2	241	21	AAC80397	HLA-A intron 2 seq
c 831	14	6.2	241	21	AAC80398	HLA-A intron 2 seq
c 832	14	6.2	241	21	AAC80399	HLA-A intron 2 seq
c 833	14	6.2	241	21	AAC80400	HLA-A intron 2 seq
c 834	14	6.2	241	21	AAC80401	HLA-A intron 2 seq
c 835	14	6.2	241	21	AAC80403	HLA-A intron 2 seq
c 836	14	6.2	241	21	AAC80404	HLA-A intron 2 seq
c 837	14	6.2	241	21	AAC80405	HLA-A intron 2 seq
c 838	14	6.2	241	21	AAC80406	HLA-A intron 2 seq
c 839	14	6.2	241	21	AAC80411	HLA-A intron 2 seq
c 840	14	6.2	241	21	AAC80412	HLA-A intron 2 seq
c 841	14	6.2	241	21	AAC80413	HLA-A intron 2 seq
c 842	14	6.2	241	21	AAC80414	HLA-A intron 2 seq
c 843	14	6.2	241	21	AAC80415	HLA-A intron 2 seq
c 844	14	6.2	241	21	AAC80416	HLA-A intron 2 seq
c 845	14	6.2	241	21	AAC80417	HLA-A intron 2 seq
c 846	14	6.2	241	21	AAC80418	HLA-A intron 2 seq
c 847	14	6.2	241	21	AAC80419	HLA-A intron 2 seq
c 848	14	6.2	241	21	AAC80420	HLA-A intron 2 seq
c 849	14	6.2	241	21	AAC80421	HLA-A intron 2 seq
c 850	14	6.2	241	21	AAC80422	HLA-A intron 2 seq
c 851	14	6.2	241	21	AAC80423	HLA-A intron 2 seq
c 852	14	6.2	241	21	AAC80424	HLA-A intron 2 seq
c 853	14	6.2	241	21	AAC80425	HLA-A intron 2 seq
c 854	14	6.2	242	18	AAV02664	Human HLA-A gene i
c 855	14	6.2	242	21	AAA11040	Consensus sequence
856	14	6.2	245	22	ABA50623	Human breast cell
c 857	14	6.2	246	22	AAK24351	Human brain expres
c 858	14	6.2	246	22	AAK50364	Human bone marrow
c 859	14	6.2	246	22	AAI56341	Probe #25027 used
c 860	14	6.2	249	21	AAA36806	Human dysferlin re
c 861	14	6.2	249	21	AAX82897	Human dysferlin DN
862	14	6.2	250	21	AAC16870	Human secreted pro
c 863	14	6.2	261	21	AAA59492	5' sequence of DNA
c 864	14	6.2	263	23	AAS87969	DNA encoding novel
c 865	14	6.2	269	21	AAA44313	Human secreted exp
866	14	6.2	274	18	AAV02823	Human RHAMM genomi
c 867	14	6.2	283	22	AAS27902	Novel cDNA encodin
868	14	6.2	283	22	AAK82963	Human immune/haema
869	14	6.2	293	22	AAK58853	Human immune/haema
870	14	6.2	293	22	AAK73879	Human immune/haema
871	14	6.2	293	22	AAK73880	Human immune/haema
872	14	6.2	300	20	AAZ14137	Human gene express
873	14	6.2	300	21	AAA01326	Human colon cancer
874	14	6.2	301	22	AAD21716	Human stem cell gr
875	14	6.2	304	21	AAC05413	Human secreted pro
c 876	14	6.2	307	22	ABA11517	Human nervous syst
c 877	14	6.2	309	20	AAV90041	EST clone CW481.
878	14	6.2	311	22	AAK68345	Human immune/haema
879	14	6.2	314	21	AAF10270	Fusarium venenatum
c 880	14	6.2	322	22	AAS23191	DNA encoding novel
c 881	14	6.2	325	22	ABA48607	Human breast cell
c 882	14	6.2	325	22	ABA66517	Human foetal liver
c 883	14	6.2	325	22	ABA33581	Probe #12047 for g
c 884	14	6.2	325	22	AAK14941	Human brain expres
c 885	14	6.2	325	22	AAK40674	Human bone marrow
c 886	14	6.2	325	22	AAI21438	Probe #11371 for g
c 887	14	6.2	325	22	AAI46727	Probe #15413 used
c 888	14	6.2	325	22	AAI07133	Probe #7124 used t
889	14	6.2	330	21	AAC23145	Human secreted pro
890	14	6.2	332	22	AAI88816	Human polynucleoti
891	14	6.2	334	22	AAK56289	Human immune/haema
c 892	14	6.2	339	20	AAZ19382	M. tuberculosis an
c 893	14	6.2	339	20	AAZ19170	M. tuberculosis re
c 894	14	6.2	339	22	AAS03814	M. tuberculosis an
c 895	14	6.2	347	22	AAK72458	Human immune/haema
c 896	14	6.2	347	22	AAK72459	Human immune/haema
c 897	14	6.2	347	22	AAK72460	Human immune/haema
c 898	14	6.2	350	22	AAS35835	Human cardiovascul
c 899	14	6.2	350	22	AAK58317	Human immune/haema
900	14	6.2	358	19	AAV66399	cDNA clone H47990.
c 901	14	6.2	359	21	AAC03546	Human secreted pro
902	14	6.2	361	22	ABA48981	Human breast cell
903	14	6.2	361	22	ABA33974	Probe #12440 for g
904	14	6.2	361	22	AAI21826	Probe #11759 for g
905	14	6.2	361	22	AAI47112	Probe #15798 used
906	14	6.2	361	22	AAI07513	Probe #7504 used t
907	14	6.2	369	14	AAQ59994	Human brain Expres
c 908	14	6.2	369	22	ABA50866	Human breast cell
c 909	14	6.2	369	22	ABA68840	Human foetal liver
c 910	14	6.2	369	22	ABA35790	Probe #14256 for g
c 911	14	6.2	369	22	AAK17175	Human brain expres
c 912	14	6.2	369	22	AAK42958	Human bone marrow
c 913	14	6.2	369	22	AAI23723	Probe #13656 for g
c 914	14	6.2	369	22	AAI49036	Probe #17722 used
c 915	14	6.2	369	22	AAI09339	Probe #9330 used t
c 916	14	6.2	371	22	AAK88949	Human digestive sy
917	14	6.2	372	16	AAT26549	Human gene signatu
918	14	6.2	377	19	AAV17747	Human breast cance
c 919	14	6.2	377	22	AAI81618	Human polynucleoti
c 920	14	6.2	378	22	AAK63042	Human immune/haema
921	14	6.2	382	22	AAI84492	Human polynucleoti
922	14	6.2	384	22	AAL17650	Human breast cance
923	14	6.2	384	22	AAL18686	Human breast cance
924	14	6.2	385	22	AAL10922	Human breast cance
925	14	6.2	389	21	AAA80652	Human secreted pro
926	14	6.2	390	22	AAF65045	Novel human polynu
927	14	6.2	393	22	AAF66699	Novel human polynu
928	14	6.2	394	14	AAQ60760	Human brain Expres
929	14	6.2	395	22	AAI86496	Human polynucleoti
930	14	6.2	398	22	AAI83317	Human polynucleoti
c 931	14	6.2	399	20	AAX41514	Human secreted pro
932	14	6.2	401	22	AAK95984	Human neuregulin g
933	14	6.2	401	22	AAK97477	Human neuregulin g
c 934	14	6.2	401	22	AAS40316	DNA encoding human
c 935	14	6.2	401	22	AAL03916	Human reproductive
936	14	6.2	404	21	AAC08931	Human secreted pro
c 937	14	6.2	405	21	AAC25365	Human secreted pro
938	14	6.2	406	22	AAL20753	Human breast cance
939	14	6.2	406	23	AAS84227	DNA encoding novel
940	14	6.2	407	22	AAF66214	Novel human polynu
941	14	6.2	408	22	AAL11863	Human breast cance
c 942	14	6.2	408	22	AAI91810	Human polynucleoti
c 943	14	6.2	413	22	AAL23872	Human breast cance
944	14	6.2	413	22	AAI92167	Human polynucleoti
c 945	14	6.2	414	22	AAL15019	Human breast cance
c 946	14	6.2	416	21	AAZ29486	Incyte clone 12110
c 947	14	6.2	416	22	ABA72539	Human foetal liver
c 948	14	6.2	416	22	ABA38282	Probe #16748 for g
c 949	14	6.2	416	22	AAK20963	Human brain expres
c 950	14	6.2	416	22	AAK47116	Human bone marrow
c 951	14	6.2	416	22	AAI52952	Probe #21638 used
c 952	14	6.2	416	23	AAS87970	DNA encoding novel
953	14	6.2	417	21	AAC22774	Human secreted pro
954	14	6.2	418	22	ABA45497	Human breast cell
955	14	6.2	422	23	AAS66872	DNA encoding novel
c 956	14	6.2	425	22	AAS39470	cDNA encoding nove
c 957	14	6.2	425	22	AAK88337	Human digestive sy
c 958	14	6.2	427	22	AAK73686	Human immune/haema

c 959	14	6.2	427	22	AAK73687	Human immune/haema
c 960	14	6.2	430	22	AAL26228	Human breast cance
961	14	6.2	431	22	AAI81528	Human polynucleoti
c 962	14	6.2	431	22	AAH23701	Human TSG16 altern
c 963	14	6.2	433	21	AAC18224	Human secreted pro
964	14	6.2	435	22	AAL10575	Human breast cance
c 965	14	6.2	438	22	AAL24370	Human breast cance
c 966	14	6.2	439	22	AAH35537	Human colon cancer
c 967	14	6.2	441	21	AAC17357	Human secreted pro
968	14	6.2	442	22	AAL05342	Human reproductive
c 969	14	6.2	442	22	AAI88119	Human polynucleoti
970	14	6.2	443	22	AAL05343	Human reproductive
971	14	6.2	443	22	AAI56170	Probe #24856 used
c 972	14	6.2	444	22	AAK60629	Human immune/haema
973	14	6.2	449	22	AAL01530	Human reproductive
c 974	14	6.2	450	22	ABA43707	Human breast cell
c 975	14	6.2	450	22	ABA54164	Human foetal liver
c 976	14	6.2	450	22	ABA23909	Probe #2375 for ge
c 977	14	6.2	450	22	AAK02434	Human brain expres
c 978	14	6.2	450	22	AAK27875	Human bone marrow
c 979	14	6.2	450	22	AAI12456	Probe #2389 for ge
c 980	14	6.2	450	22	AAI33810	Probe #2496 used t
c 981	14	6.2	450	22	AAI02367	Probe #2358 used t
c 982	14	6.2	455	22	ABA43495	Human breast cell
c 983	14	6.2	455	22	ABA53943	Human foetal liver
c 984	14	6.2	455	22	ABA23694	Probe #2160 for ge
c 985	14	6.2	455	22	AAK02213	Human brain expres
c 986	14	6.2	455	22	AAK27660	Human bone marrow
987	14	6.2	455	22	AAK30316	Human bone marrow
c 988	14	6.2	455	22	AAI12241	Probe #2174 for ge
989	14	6.2	455	22	AAI14920	Probe #4853 for ge
c 990	14	6.2	455	22	AAI33595	Probe #2281 used t
c 991	14	6.2	455	22	AAI02154	Probe #2145 used t
992	14	6.2	455	22	AAI04697	Probe #4688 used t
c 993	14	6.2	456	24	ABA02988	Human ubiquitin co
994	14	6.2	458	21	AAA31094	Plant microsatelli
995	14	6.2	458	22	AAS47119	Human breast cance
996	14	6.2	458	22	AAF17689	Human breast cance
c 997	14	6.2	459	22	ABA57002	Human foetal liver
c 998	14	6.2	459	22	AAK05066	Human brain expres
c 999	14	6.2	459	22	AAK30616	Human bone marrow
c1000	14	6.2	461	22	ABA55533	Human foetal liver

ALIGNMENTS

RESULT 1
AAQ32362
ID AAQ32362 standard; DNA; 225 BP.
XX
AC AAQ32362;
XX
DT 22-APR-1993 (first entry)
XX
DE MAGE-6 gene.
XX
KW Melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
XX
OS Homo sapiens.
XX
PN WO9220356-A.
XX
PD 26-NOV-1992.
XX
PF 22-MAY-1992; 92WO-US04354.
XX
PR 23-MAY-1991; 91US-0705702.
PR 09-JUL-1991; 91US-0728838.
PR 23-SEP-1991; 91US-0764364.
PR 12-DEC-1991; 91US-0807043.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI Van Den Eynde B, Van Der Bruggen P, Van Pel A;
XX
DR WPI; 1992-415460/50.
XX
PT Nucleic acid mol. encoding a human tumour rejection antigen
PT precursor - useful as an immunostimulant in a vaccine for
PT treating and preventing cancers, also useful in diagnosis
XX
PS Disclosure; Page 88; 142pp; English.
XX
CC The sequences given in AAQ32352-69 represent a new family of genes
CC refered to as melanoma antigens (MAGE). The cDNAs of this gene
CC family were identified during the isolation of the antigen E gene.
CC The MAGE cDNAs, when tested, did not transfer expression of antigen
CC E, but they did show substantial homology to the antigen E cDNA
CC sequence. The MAGE DNAs share a certain degree of homology with each
CC other and are expressed in tumour cells including several types of
CC human tumor cells as well as in human tumors. MAGE expression is not
CC restricted to melanomas. MAGE refers to a family of tumor rejection
CC antigen precursors. The antigens resulting from these genes are
CC referred to as MAGE TRAs or melanoma antigen tumor rejection antigens.
CC See also AAQ32351.
XX
SQ Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 13; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.1e-105;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 TATTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 tatttctttcctgtgatcttcagcaaagcttccgattccttgcagctggtctttggcatc 60

Qy     61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gagctgatggaagtggaccccatcggccacgtgtacatctttgccacctgcctgggcctc 120

Qy    121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAGGACAGGCTTCCTGATAATC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 tcctacgatggcctgctgggtgacaatcagatcatgcccaggacaggcttcctgataatc 180

Qy    181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCTGAGGAG 225
          |||||||||||||||||||||||||||||||||||||||||||||
Db    181 atcctggccataatcgcaagagagggcgactgtgcccctgaggag 225
```

RESULT 2
AAQ72487
ID AAQ72487 standard; cDNA to mRNA; 225 BP.
XX
AC AAQ72487;
XX
DT 22-JUN-1995 (first entry)
XX
DE Tumour rejection antigen MAGE-6 cDNA.
XX
KW Tumour rejection antigen; melanoma antigen-6; MAGE-6; MAGE-3;
KW cancer; cytolytic T cells; antigen D; human leucocyte antigen;
KW ss.
XX
OS Homo sapiens.
XX
PN WO9423031-A.
XX
PD 13-OCT-1994.
XX
PF 17-MAR-1994; 94WO-US02877.
XX
PR 26-MAR-1993; 93US-0037230.

```
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Boon-falleur T,  Gaugler B,  Van DEN EYNDE B,  Van DER BRUGGEN P;
XX
DR   WPI; 1994-333192/41.
XX
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
XX
PS   Example 32; Page 73; 105pp; English.
XX
CC   AAQ72487 is the cDNA sequence which codes for melanoma antigen-6
CC   (MAGE-6). Another melanoma antigen MAGE-3 is encoded by
CC   AAQ72470, this is a tumour rejection antigen precursor. Melanomas
CC   characterised by the expression of MAGE-3 can be detected, or
CC   monitored, by contacting a test sample with an agent that can
CC   recognise MAGE-3. The melanoma can be treated by the administration
CC   of cytolytic T cells specific for the complex of antigen D (the
CC   mature rejection antigen derived from MAGE-3) and a human leucocyte
CC   antigen (esp. HLA-A1).
XX
SQ   Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;


  Query Match             100.0%;  Score 225;  DB 15;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-105;
  Matches  225;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TATTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 tatttctttcctgtgatcttcagcaaagcttccgattccttgcagctggtctttggcatc 60

Qy      61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 gagctgatggaagtggaccccatcggccacgtgtacatctttgccacctgcctgggcctc 120

Qy     121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAGGACAGGCTTCCTGATAATC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tcctacgatggcctgctgggtgacaatcagatcatgcccaggacaggcttcctgataatc 180

Qy     181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCTGAGGAG 225
            |||||||||||||||||||||||||||||||||||||||||||||
Db     181 atcctggccataatcgcaagagagggcgactgtgcccctgaggag 225


RESULT   3
AAX84122
ID   AAX84122 standard; cDNA; 225 BP.
XX
AC   AAX84122;
XX
DT   08-SEP-1999  (first entry)
XX
DE   MAGE-6 gene.
XX
KW   Tumour rejection antigen; vaccine; cancer; MAGE-6 gene; ss.
XX
OS   Homo sapiens.
XX
PN   US5925729-A.
XX
PD   20-JUL-1999.
XX
PF   02-MAY-1994;   94US-0142368.
XX
PR   02-MAY-1994;   94US-0142368.
PR   23-MAY-1991;   91US-0705702.
PR   09-JUL-1991;   91US-0728838.
PR   23-SEP-1991;   91US-0764365.
PR   12-DEC-1991;   91US-0807043.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Boon T,  Chomez P,  De Plaen E,  Lurquin C,  Traversari C;
PI   Van Den Eynde B, Van Der Bruggen P,  Van Pel A;
XX
DR   WPI; 1999-418294/35.
XX
PT   New tumour rejection antigen is useful as a vaccine against
PT   cancerous diseases
XX
PS   Disclosure; Column 69-70; 58pp; English.
XX
CC   This sequence represents the MAGE-6 gene sequence.
CC   The invention relates to a tumour rejection antigen sequence that is
CC   useful as a tumour rejection antigen for vaccination against cancerous
CC   conditions.
XX
SQ   Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;


  Query Match             100.0%;  Score 225;  DB 20;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-105;
  Matches  225;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TATTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 tatttctttcctgtgatcttcagcaaagcttccgattccttgcagctggtctttggcatc 60

Qy      61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 gagctgatggaagtggaccccatcggccacgtgtacatctttgccacctgcctgggcctc 120

Qy     121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAGGACAGGCTTCCTGATAATC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tcctacgatggcctgctgggtgacaatcagatcatgcccaggacaggcttcctgataatc 180

Qy     181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCTGAGGAG 225
            |||||||||||||||||||||||||||||||||||||||||||||
Db     181 atcctggccataatcgcaagagagggcgactgtgcccctgaggag 225


RESULT   4
AAT01166
ID   AAT01166 standard; DNA; 225 BP.
XX
AC   AAT01166;
XX
DT   26-FEB-1996  (first entry)
XX
DE   MAGE-6 gene.
XX
KW   MAGE-6; melanoma; tumour rejection antigen; cancer; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9523874-A1.
XX
PD   08-SEP-1995.
XX
PF   23-FEB-1995;   95WO-US02203.
XX
PR   30-NOV-1994;   94US-0346774.
PR   01-MAR-1994;   94US-0204727.
PR   10-MAR-1994;   94US-0209172.
PR   01-SEP-1994;   94US-0299849.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Boon-Falleur T,  Brasseur F,  Chomez P,  De Plaen E;
PI   De Smet C,  Gaugler B, Lethe B,  Marchand M,  Patard J;
PI   Szikora J,  Van Den Eynde B,  Van Derbruggen P,  Weynants P;
XX
DR   WPI; 1995-320586/41.
XX
```

PT Determn. of cancerous condition(s) - using a nucleic acid as a
PT primer to determine expression of a MAGE tumour rejection antigen
PT precursor
XX
PS Example 32; Page 80; 121pp; English.
XX
CC A family of human tumour rejection antigen precursor, MAGE, genes
CC (AAT05091-99, AAT01165-71) was isolated from various tumour cell lines.
CC cDNA (AAT01166) coding for MAGE-6 was obtd. from human melanoma
CC LB-33-MEL cells. MAGE serve as markers for tumour diagnosis. The
CC genes are silent in normal cells.
XX
SQ Sequence 225 BP; 44 A; 66 C; 57 G; 58 T; 0 other;

Query Match 77.3%; Score 174; DB 16; Length 225;
Best Local Similarity 99.6%; Pred. No. 3.6e-79;
Matches 224; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TATTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
Db 1 tatttctttcctgtgatcttcagcaaagcttccgattccttgcagctggtctttggcatc 60

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 61 gagctgatggaagtggaccccatcggccacgtgtacatctttgccacctgcctgggcctc 120

Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAGGACAGGCTTCCTGATAATC 180
Db 121 tcctacgatggcctgctgggtgacaatcagatcatccccaggacaggcttcctgataatc 180

Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCTGAGGAG 225
Db 181 atcctggccataatcgcaagagagggcgactgtgcccctgaggag 225

RESULT 5
AAX87596
ID AAX87596 standard; cDNA; 1362 BP.
XX
AC AAX87596;
XX
DT 26-OCT-1999 (first entry)
XX
DE CLYTA-MAGE-3-His fusion DNA.
XX
KW MAGE-3; CLYTA-MAGE-3-His; fusion protein; tumour; melanoma;
KW breast cancer; bladder cancer; lung cancer; colon cancer;
KW head and squamous cell carcinoma; oesophagus carcinoma; vaccine;
KW human; ss.
XX
OS Chimeric - Streptococcus pneumoniae.
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX
PN WO9940188-A2.
XX
PD 12-AUG-1999.
XX
PF 02-FEB-1999; 99WO-EP00660.
XX
PR 06-FEB-1998; 98GB-0002650.
PR 05-FEB-1998; 98GB-0002543.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX
DR WPI; 1999-494293/41.
DR P-PSDB; AAY06593.
XX
PT New protein derivatives used in cancer vaccine therapy for treating
PT a range of cancers including melanomas, carcinomas and cancers of
PT breast
XX
PS Example 10; Page 72; 72pp; English.
XX
CC This DNA sequence codes for a fusion protein (see AAY06593) composed
CC of the C-terminal portion of the Streptococcus pneumoniae LYTA
CC protein (CLYTA), the human MAGE-3 tumour-associated antigen and a
CC hexahistidine tail. A vector designed for recombinant expression
CC of the fusion protein in Escherichia coli is provided. The CLYTA
CC moiety provides expression of soluble fusion protein, facilitates
CC affinity purification of the fusion protein, and also acts as a
CC T-helper epitope. The invention relates to MAGE proteins fused to
CC an immunological fusion partner, e.g. Clyta-MAGE-3-His. These novel
CC fusion proteins provide vaccines for immunotherapy of melanomas or
CC other MAGE-associated tumours like breast, bladder, lung and
CC non-small cell lung cancer, head and squamous cell carcinoma, colon
CC carcinoma and oesophagus carcinoma.
XX
SQ Sequence 1362 BP; 345 A; 348 C; 383 G; 286 T; 0 other;

Query Match 69.8%; Score 157; DB 20; Length 1362;
Best Local Similarity 100.0%; Pred. No. 1.8e-70;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
Db 826 ttctttcctgtgatcttcagcaaagcttccgattccttgcagctggtctttggcatcgag 885

Qy 64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
Db 886 ctgatggaagtggaccccatcggccacgtgtacatctttgccacctgcctgggcctctcc 945

Qy 124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
Db 946 tacgatggcctgctgggtgacaatcagatcatgccca 982

RESULT 6
AAV22716
ID AAV22716 standard; DNA; 1375 BP.
XX
AC AAV22716;
XX
DT 18-AUG-1998 (first entry)
XX
DE MAGE-6 cDNA.
XX
KW Human tumor rejection antigen precursor; TRA; MAGE-6; HLA-Cw*16;
KW major histocompatibility complex; MHC; cytotoxic T-cell; ss.
XX
OS Homo sapiens.
XX
PN WO9810780-A1.
XX
PD 19-MAR-1998.
XX
PF 27-AUG-1997; 97WO-US15069.
XX
PR 13-SEP-1996; 96US-0713354.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, DePlaen E, Van Der Bruggen P;
XX
DR WPI; 1998-207144/18.
XX
PT Tumour rejection antigen precursor, MAGE-6 derived peptide(s) which
PT bind to HLA-Cw*16 - used for provoking proliferation of cytotoxic T
PT cells, useful for, e.g. treatment of cancerous cells
XX
PS Disclosure; Page 19; 31pp; English.
XX

```
CC   The present sequence represents a MAGE-6 cDNA encoding a human tumor
CC   rejection antigen (TRA) precursor.  The invention provides for TRAs
CC   (AAW56268-W56272) which are processed from TRA precursors that are
CC   derived from the MAGE-6 gene.  The TRAs bind to major histocompatibility
CC   complex (MHC) molecules of the type HLA-Cw*16 to provoke a cytotoxic
CC   T-cell response against cells exhibiting this particular TRA-MHC
CC   complex. As the cells presenting these complexes are human cancerous
CC   cells, the TRA peptides are claimed to be useful in provoking lysis of
CC   these cancerous cells thereby providing a probable method of treating
CC   cancer.
XX
SQ   Sequence 1375 BP; 293 A; 364 C; 404 G; 314 T; 0 other;


  Query Match             69.8%;  Score 157;  DB 19;  Length 1375;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-70;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     595 ttctttcctgtgatcttcagcaaagcttccgattccttgcagctggtctttggcatcgag 654

Qy      64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     655 ctgatggaagtggaccccatcggccacgtgtacatctttgccacctgcctgggcctctcc 714

Qy     124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
           |||||||||||||||||||||||||||||||||||||
Db     715 tacgatggcctgctgggtgacaatcagatcatgccca 751


RESULT   7
AAS02056
ID   AAS02056 standard; cDNA; 4204 BP.
XX
AC   AAS02056;
XX
DT   16-JUL-2001  (first entry)
XX
DE   DNA encoding molecule for disease detection and treatment, mddt21.
XX
KW   Human; mddt21; gene therapy; adenosine deaminase deficiency;
KW   ADA; severe combined immunodeficiency syndrome; cystic fibrosis;
KW   thalassaemia; familial hypercholesterolaemia; haemophilia; factor VIII;
KW   factor IX; cancer; cell proliferation; parasite; human retrovirus; HIV;
KW   hepatitis B; hepatitis C; Candida albicans; Plasmodinium falciparum;
KW   Paracoccidioides brasiliensis; Trypanosoma brasiliensis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200123538-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US26085.
XX
PR   28-SEP-1999;   99US-0156565.
PR   30-NOV-1999;   99US-0168197.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Hodgson DM,  Lincoln SE,  Russo FD,  Spiro PA,  Banville SC;
PI   Bratcher SR,  Dufour GE,  Cohen HJ,  Rosen BH,  Shah P,  Chalup MS;
PI   Hillman JL,  Jones AL,  Yu JY,  Greenawalt LB,  Panzer SR;
PI   Roseberry AM,  Wright RJ,  Chen W,  Liu TF,  Yap PE,  Stockdreher TK;
PI   Amshey S,  Fong WT;
XX
DR   WPI; 2001-258131/26.
XX
PT   Purified disease treatment and detection molecule polynucleotides and
PT   polypeptides, useful for providing diagnostic assays and gene therapy -
XX
PS   Claim 1; Page 109-110; 113pp; English.
XX
CC   The sequence represents the coding sequence of molecule for disease
CC   detection and treatment, mddt21, shown by computer analysis to be similar
CC   to the MAGE family of proteins. The sequence may be used for
CC   somatic or germline gene therapy. Gene therapy may be performed to: (i)
CC   correct genetic deficiency such as in severe combined immunodeficiency
CC   syndrome associated with adenosine deaminase (ADA) deficiency, cystic
CC   fibrosis, thalassaemias, familial hypercholesterolaemia and haemophilia
CC   caused by factor VIII or factor IX deficiencies; (ii) express a
CC   conditional lethal gene product (such as in the case of cancers which
CC   result from unregulated cell proliferation); (iii) express a protein
CC   which affords protection against intracellular parasites (for example,
CC   human retroviruses such as HIV, hepatitis B or C, fungal parasites such
CC   as Candida albicans and Paracoccidioides brasiliensis, and protozoal
CC   parasites such as Plasmodinium falciparum and Trypanosoma brasiliensis.
XX
SQ   Sequence 4204 BP; 947 A; 1145 C; 1219 G; 893 T; 0 other;


  Query Match             69.8%;  Score 157;  DB 22;  Length 4204;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-70;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2900 ttctttcctgtgatcttcagcaaagcttccgattccttgcagctggtctttggcatcgag 2959

Qy      64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2960 ctgatggaagtggaccccatcggccacgtgtacatctttgccacctgcctgggcctctcc 3019

Qy     124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
           |||||||||||||||||||||||||||||||||||||
Db    3020 tacgatggcctgctgggtgacaatcagatcatgccca 3056


RESULT   8
AAD18141
ID   AAD18141 standard; cDNA; 666 BP.
XX
AC   AAD18141;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human melanoma associated antigen 3 (MAGE-3) truncated cDNA.
XX
KW   Human; melanoma associated antigen 3; MAGE-3; neuroprotective; nootropic;
KW   immunosuppressive; caspase-12 activation; cell death related disease;
KW   cell death inhibitor; cancer-specific protein; Alzheimer's disease;
KW   neurodegenerative disease; autoimmune disease; amyotrophy; gene therapy;
KW   organ disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..666
FT                   /*tag= a
FT                   /product= "Human MAGE-3 protein"
FT                   /note= "CDS does not include start codon"
FT                   /partial
XX
PN   EP1126027-A1.
XX
PD   22-AUG-2001.
XX
PF   16-FEB-2001; 2001EP-0301361.
XX
PR   18-FEB-2000; 2000JP-0041927.
XX
PA   (RIKE ) RIKEN KK.
XX
PI   Morishima N,  Shibata T;
XX
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```
DR   WPI; 2001-591501/67.
DR   P-PSDB; AAE10673.
XX
PT   New polypeptide for treating cell death related diseases such as
PT   Alzheimer's disease, neurodegenerative diseases, autoimmune diseases,
PT   amyotrophy and organ disorders comprises the recombinant
PT   cancer-specific protein MAGE-3 -
XX
PS   Claim 3; Page 25-27; 41pp; English.
XX
CC   The present sequence is the truncated form of human melanoma
CC   associated antigen 3 (MAGE-3) cDNA. The present invention relates
CC   to MAGE-3 protein or its truncated form which specifically bind to
CC   caspase-12 or pro-caspase-12 protein and inhibit their activation.
CC   MAGE-3 proteins are cancer-specific proteins and are used as cell-
CC   death inhibitors. Therapeutic agents comprising MAGE-3 sequence are
CC   useful for treating cell death related diseases such as Alzheimer's
CC   disease, neurodegenerative diseases, autoimmune diseases, amyotrophy
CC   and organ disorders. MAGE-3 gene is useful as an agent for gene therapy.
CC   The sequences of the invention are useful for preventing or treating a
CC   cell death-related disease developing in tissues in the nervous system,
CC   vascular system, respiratory system, digestive system, lymph system,
CC   urinary system, or reproductive system.
XX
SQ   Sequence 666 BP; 151 A; 165 C; 197 G; 153 T; 0 other;


  Query Match             32.9%;  Score 74;  DB 22;  Length 666;
  Best Local Similarity   99.2%;  Pred. No. 4.8e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     189 ttccttgcagctggtctttggcatcgagctgatggaagtggaccccatcggccacttgta 248

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     249 catctttgccacctgcctgggcctctcctacgatggcctgctgggtgacaatcagatcat 308

Qy     156 GCCCA 160
           |||||
Db     309 gccca 313


RESULT   9
AAD12993
ID   AAD12993 standard; DNA; 945 BP.
XX
AC   AAD12993;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human MAGE-A3 DNA.
XX
KW   MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;
KW   tumour cell; immunostimulant; antigen presentation; cancer; melanoma;
KW   CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma;
KW   myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic;
KW   gene therapy; human; MAGE-A3; tumour rejection antigen; TRA; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..945
FT                   /*tag=  a
FT                   /product= "MAGE-A3 protein"
XX
PN   WO200153833-A1.
XX
PD   26-JUL-2001.
XX
PF   19-JAN-2001; 2001WO-US02008.
XX
PR   20-JAN-2000; 2000US-0177242.
PR   25-OCT-2000; 2000US-0243212.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Luiten R,  Boon-Falleur T,  Van Der Bruggen P,  Stroobant V;
PI   Demotte N,  Schultz E;
XX
DR   WPI; 2001-488724/53.
DR   P-PSDB; AAE06853.
XX
PT   Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or
PT   HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used
PT   in diagnosis and treatment of a disorder characterized by expression of
PT   MAGE-A1 or -A3 -
XX
PS   Example 3; Page 94-95; 103pp; English.
XX
CC   The invention relates to functional variants and isolated mimetics of a
CC   MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide,
CC   or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described
CC   in the specification. MAGE genes encode tumour rejection antigens
CC   (TRAs) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules.
CC   The MAGE antigenic peptide acts by binding to HLA molecules
CC   on tumour cells and stimulating recognition of these cells and thus
CC   signalling them to the immune system for destruction. The peptide when
CC   presented by HLA molecule induces the activation and stimulation of
CC   CD8+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to
CC   treat and diagnose disorders characterised by expression of MAGE-A1
CC   or -A3. Disorders include cancers e.g melanomas, oesophageal, lung,
CC   head and neck, breast, colorectal, prostate, renal, bladder,
CC   hepatocellular, papillary thyroid and gastric carcinomas, myelomas,
CC   brain tumours, sarcomas, seminomas, and ovarian tumours. The present
CC   sequence is human MAGE-A3 DNA.
XX
SQ   Sequence 945 BP; 210 A; 254 C; 278 G; 203 T; 0 other;


  Query Match             32.9%;  Score 74;  DB 22;  Length 945;
  Best Local Similarity   99.2%;  Pred. No. 4.9e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     468 ttccttgcagctggtctttggcatcgagctgatggaagtggaccccatcggccacttgta 527

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     528 catctttgccacctgcctgggcctctcctacgatggcctgctgggtgacaatcagatcat 587

Qy     156 GCCCA 160
           |||||
Db     588 gccca 592


RESULT  10
AAX87592
ID   AAX87592 standard; cDNA; 1212 BP.
XX
AC   AAX87592;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Haemagglutinin-MAGE-3-His fusion DNA.
XX
KW   MAGE-3; haemagglutinin; NS1-MAGE-3-His; fusion protein; tumour;
KW   melanoma; breast cancer; bladder cancer; lung cancer;
KW   head and squamous cell carcinoma; colon cancer;
KW   oesophagus carcinoma; vaccine; human; ss.
XX
OS   Chimeric - Influenza virus.
OS   Chimeric - Homo sapiens.
OS   Chimeric - synthetic.
```

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XX
PN   WO9940188-A2.
XX
PD   12-AUG-1999.
XX
PF   02-FEB-1999;   99WO-EP00660.
XX
PR   06-FEB-1998;   98GB-0002650.
PR   05-FEB-1998;   98GB-0002543.
XX
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Cabezon Silva T,  Cohen J,  Slaoui MM,  Vinals Bassols C;
XX
DR   WPI; 1999-494293/41.
DR   P-PSDB; AAY06591.
XX
PT   New protein derivatives used in cancer vaccine therapy for treating
PT   a range of cancers including melanomas, carcinomas and cancers of
PT   breast
XX
PS   Example 7; Page 69; 72pp; English.
XX
CC   This DNA sequence codes for a fusion protein (see AAY06591) composed
CC   of haemagglutinin NS1 of influenza virus, the human MAGE-3
CC   tumour-associated antigen and a hexahistidine tail.  A vector
CC   designed for recombinant expression of the fusion protein is
CC   provided.  MAGE-3 cDNA was amplified using primers that altered the
CC   first 5 codons to Escherichia coli codon usage.  The NS1 moiety
CC   provided the fusion protein with additional exogenous T-helper
CC   epitopes.  The invention relates to MAGE proteins fused to an
CC   immunological fusion partner, e.g. NS1-MAGE-3-His.  These novel
CC   fusion proteins provide vaccines for immunotherapy of melanomas or
CC   other MAGE-associated tumours like breast, bladder, lung and
CC   non-small cell lung cancer, head and squamous cell carcinoma, colon
CC   carcinoma and oesophagus carcinoma.
XX
SQ   Sequence 1212 BP; 289 A; 319 C; 344 G; 260 T; 0 other;


  Query Match             32.9%;  Score 74;  DB 20;  Length 1212;
  Best Local Similarity   99.2%;  Pred. No. 4.9e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     708 ttccttgcagctggtctttggcatcgagctgatggaagtggaccccatcggccacttgta 767

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     768 catctttgccacctgcctgggcctctcctacgatggcctgctgggtgacaatcagatcat 827

Qy     156 GCCCA 160
           |||||
Db     828 gccca 832


RESULT  11
AAX87588
ID   AAX87588 standard; cDNA; 1353 BP.
XX
AC   AAX87588;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Lipoprotein D-MAGE-3-His fusion DNA.
XX
KW   MAGE-3; lipoprotein D; LPD-MAGE-3-His; fusion protein; tumour;
KW   melanoma; breast cancer; bladder cancer; lung cancer;
KW   head and squamous cell carcinoma; colon cancer;
KW   oesophagus carcinoma; vaccine; human; ss.
XX
OS   Chimeric - Haemophilus influenzae.
OS   Chimeric - Homo sapiens.
OS   Chimeric - synthetic.
XX
PN   WO9940188-A2.
XX
PD   12-AUG-1999.
XX
PF   02-FEB-1999;   99WO-EP00660.
XX
PR   06-FEB-1998;   98GB-0002650.
PR   05-FEB-1998;   98GB-0002543.
XX
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Cabezon Silva T,  Cohen J,  Slaoui MM,  Vinals Bassols C;
XX
DR   WPI; 1999-494293/41.
DR   P-PSDB; AAY06589.
XX
PT   New protein derivatives used in cancer vaccine therapy for treating
PT   a range of cancers including melanomas, carcinomas and cancers of
PT   breast
XX
PS   Example 1; Page 66; 72pp; English.
XX
CC   This DNA sequence codes for a fusion protein (see AAY06589) composed
CC   of lipidated protein D (LPD) of Haemophilus influenzae B, the human
CC   MAGE-3 tumour-associated antigen and a hexahistidine tail.  A
CC   vector designed for recombinant expression of the fusion protein is
CC   provided.  MAGE-3 cDNA was amplified using primers that altered the
CC   first 5 codons to Escherichia coli codon usage.  The LPD moiety
CC   provided the fusion protein with additional exogenous T-cell
CC   epitopes and also increased expression levels in E. coli.  The
CC   lipid tail ensured optimal presentation of the antigen to
CC   antigen-presenting cells.  The affinity tag facilitated
CC   purification.  The invention relates to MAGE proteins fused to an
CC   immunological fusion partner, e.g. LPD-MAGE-3-His.  These novel
CC   fusion proteins provide vaccines for immunotherapy of melanomas or
CC   other MAGE-associated tumours like breast, bladder, lung and
CC   non-small cell lung cancer, head and squamous cell carcinoma, colon
CC   carcinoma and oesophagus carcinoma.
XX
SQ   Sequence 1353 BP; 342 A; 337 C; 354 G; 320 T; 0 other;


  Query Match             32.9%;  Score 74;  DB 20;  Length 1353;
  Best Local Similarity   99.2%;  Pred. No. 4.9e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    849 ttccttgcagctggtctttggcatcgagctgatggaagtggaccccatcggccacttgta 908

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 catctttgccacctgcctgggcctctcctacgatggcctgctgggtgacaatcagatcat 968

Qy     156 GCCCA 160
           |||||
Db    969 gccca 973


RESULT  12
AAQ72480
ID   AAQ72480 standard; cDNA to mRNA; 1640 BP.
XX
AC   AAQ72480;
XX
DT   22-JUN-1995  (first entry)
XX
DE   Tumour rejection antigen precursor MAGE-3 cDNA.
XX
KW   Tumour antigen rejection precursor; melanoma antigen-3; MAGE-3;
```

```
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen;
KW   P1A gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             172..1116
FT                   /*tag=  a
XX
PN   WO9423031-A.
XX
PD   13-OCT-1994.
XX
PF   17-MAR-1994;    94WO-US02877.
XX
PR   26-MAR-1993;    93US-0037230.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Boon-falleur T,  Gaugler B,  Van DEN EYNDE B,  Van DER BRUGGEN P;
XX
DR   WPI; 1994-333192/41.
XX
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
XX
PS   Example 32; Page 64; 105pp; English.
XX
CC   AAQ72480 is the P1A gene fragment which contains the cDNA coding
CC   sequence AAQ72470, which encodes melanoma antigen-3 (MAGE-3), a tumour
CC   rejection antigen precursor. Melanomas characterised by the expression of
CC   MAGE-3 can be detected, or monitored, by contacting a test sample with
CC   an agent that can recognise MAGE-3. The melanoma can be treated by the
CC   administration of cytolytic T cells specific for the complex of
CC   antigen D (the mature rejection antigen derived from MAGE-3) and a
CC   human leucocyte antigen (esp. HLA-A1).
XX
SQ   Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;


  Query Match             32.9%;  Score 74;  DB 15;  Length 1640;
  Best Local Similarity   99.2%;  Pred. No. 4.9e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     639 ttccttgcagctggtctttggcatcgagctgatggaagtggaccccatcggccacttgta 698

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     699 catctttgccacctgcctgggcctctcctacgatggcctgctgggtgacaatcagatcat 758

Qy     156 GCCCA 160
           |||||
Db     759 gccca 763


RESULT  13
AAX84116
ID   AAX84116 standard; cDNA to mRNA; 1640 BP.
XX
AC   AAX84116;
XX
DT   08-SEP-1999  (first entry)
XX
DE   MAGE-3 gene.
XX
KW   Tumour rejection antigen; vaccine; cancer; MAGE-3 gene; ss.
XX
OS   Homo sapiens.
XX
PN   US5925729-A.
XX
PD   20-JUL-1999.
XX
PF   02-MAY-1994;    94US-0142368.
XX
PR   02-MAY-1994;    94US-0142368.
PR   23-MAY-1991;    91US-0705702.
PR   09-JUL-1991;    91US-0728838.
PR   23-SEP-1991;    91US-0764365.
PR   12-DEC-1991;    91US-0807043.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Boon T,  Chomez P,  De Plaen E,  Lurquin C,  Traversari C;
PI   Van Den Eynde B, Van Der Bruggen P,  Van Pel A;
XX
DR   WPI; 1999-418294/35.
XX
PT   New tumour rejection antigen is useful as a vaccine against
PT   cancerous diseases
XX
PS   Disclosure; Column 51-54; 58pp; English.
XX
CC   This sequence represents the MAGE-3 gene sequence.
CC   The invention relates to a tumour rejection antigen sequence that is
CC   useful as a tumour rejection antigen for vaccination against cancerous
CC   conditions.
XX
SQ   Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;


  Query Match             32.9%;  Score 74;  DB 20;  Length 1640;
  Best Local Similarity   99.2%;  Pred. No. 4.9e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     639 ttccttgcagctggtctttggcatcgagctgatggaagtggaccccatcggccacttgta 698

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     699 catctttgccacctgcctgggcctctcctacgatggcctgctgggtgacaatcagatcat 758

Qy     156 GCCCA 160
           |||||
Db     759 gccca 763


RESULT  14
AAX26974
ID   AAX26974 standard; cDNA; 4204 BP.
XX
AC   AAX26974;
XX
DT   25-JUN-1999  (first entry)
XX
DE   cDNA encoding MAGE-3 polypeptide.
XX
KW   MAGE-3 tumour associated gene; human leucocyte antigen Class II;
KW   autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;
KW   osteosarcoma; leukemia; carcinoma; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             2465..3409
FT                   /*tag=  a
FT                   /product= "MAGE-3"
XX
PN   WO9914326-A1.
XX
PD   25-MAR-1999.
XX
PF   04-SEP-1998;    98WO-US18601.
```

```
XX
PR   12-SEP-1997;   97US-0928615.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYVR-) UNIV VRIJE BRUSSEL.
XX
PI   Boon-Falleur T,  Chaux P,  Corthals J,  Heirman C;
PI   Luiten R,  Stroobant V,  Thielemans K,  Van Der Bruggen P;
XX
DR   WPI; 1999-244031/20.
DR   P-PSDB; AAY01720.
XX
PT   Isolated peptides that bind to human leucocyte antigen class II
PT   molecules
XX
PS   Example 5; Page 65-67; 88pp; English.
XX
CC   The present sequence represents the MAGE-3 tumour associated gene.
CC   Peptides that bind human leucocyte antigen (HLA) Class II molecules
CC   can be derived from the MAGE-3 protein. These peptides and
CC   autologous CD4+ cells that bind to a complex of MAGE-3 peptide
CC   and HLA Class II, are used to treat MAGE-3 related diseases,
CC   particularly cancers (e.g. melanoma, osteosarcoma, leukemia and
CC   various forms of carcinoma). The peptides are also used to produce
CC   specific antibodies. Detection of of the peptides, e.g. in binding
CC   assays, particularly with antibodies, is used for diagnosis of such
CC   diseases.
XX
SQ   Sequence 4204 BP; 944 A; 1144 C; 1223 G; 893 T; 0 other;


  Query Match             32.9%;  Score 74;  DB 20;  Length 4204;
  Best Local Similarity   99.2%;  Pred. No. 5e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    2932 ttccttgcagctggtctttggcatcgagctgatggaagtggaccccatcggccacttgta 2991

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2992 catctttgccacctgcctgggcctctcctacgatggcctgctgggtgacaatcagatcat 3051

Qy     156 GCCCA 160
           |||||
Db    3052 gccca 3056


RESULT  15
AAA37927
ID   AAA37927 standard; cDNA; 4204 BP.
XX
AC   AAA37927;
XX
DT   18-AUG-2000  (first entry)
XX
DE   Human MAGE-A3 nucleotide sequence.
XX
KW   MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;
KW   cancer; human; tumour; tumour associated gene product; ss.
XX
OS   Homo sapiens.
XX
PN   WO200020581-A1.
XX
PD   13-APR-2000.
XX
PF   15-SEP-1999;   99WO-US21230.
XX
PR   05-OCT-1998;   98US-0166448.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYVR-) UNIV VRIJE BRUSSEL.
XX
PI   Chaux P,  Stroobant V,  Boon-Falleur T,  Van Der Bruggen P;
PI   Schultz ES,  Van Snick J,  Lethe B,  Thielemans K,  Corthals J;
PI   Heirman C;
XX
DR   WPI; 2000-317713/27.
DR   P-PSDB; AAB02565.
XX
PT   New MAGE-A3 class II binding peptides, useful to diagnose and treat
PT   tumours, are fragments of MAGE-A3 which bind to and are presented to T
PT   lymphocytes by human leukocyte antigen class II molecules
XX
PS   Example 6; Page 96-98; 119pp; English.
XX
CC   The present invention relates to MAGE-A3 (tumour associated gene
CC   product) human leukocyte antigen (HLA) class II-binding peptides (see
CC   AAB02566-B02595, and AAB02633-B02637). These peptides are presented to T
CC   cells in the context of HLA class II molecules. The peptides stimulate
CC   the activity and proliferation of CD4+ T lymphocytes. The invention also
CC   includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928
CC   and AAA37938-A37940). The peptides and nucleotide sequences can be used
CC   to create antibodies against the MAGE-A3 peptides, the antibodies,
CC   peptides and nucleotide sequences can be used to create a vaccine. The
CC   peptides are used to diagnose or treat a disorder characterized by
CC   expression of MAGE-3, particularly cancer. The methods can also be used
CC   in the diagnosis of disorders associated with MAGE-3 expression. Included
CC   in the invention are other human tumour antigens (see AAB02596-B02637),
CC   and PCR primers used in the course of the invention (see AAA37929-A37937
CC   and AAA37941-A37942).
XX
SQ   Sequence 4204 BP; 944 A; 1144 C; 1223 G; 893 T; 0 other;


  Query Match             32.9%;  Score 74;  DB 21;  Length 4204;
  Best Local Similarity   99.2%;  Pred. No. 5e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    2932 ttccttgcagctggtctttggcatcgagctgatggaagtggaccccatcggccacttgta 2991

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2992 catctttgccacctgcctgggcctctcctacgatggcctgctgggtgacaatcagatcat 3051

Qy     156 GCCCA 160
           |||||
Db    3052 gccca 3056


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Job time: 4450 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 02:30:46 ; Search time 63.45 Seconds
(without alignments)
871.041 Million cell updates/sec

Title: US-08-037-230D-18
Perfect score: 225
Sequence: 1 TATTTCTTTCCTGTGATCTT.....GCGACTGTGCCCCTGAGGAG 225

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	225	100.0	225	1	US-07-807-043B-15	Sequence 15, Appl
2	225	100.0	225	1	US-08-299-849B-18	Sequence 18, Appl
3	225	100.0	225	2	US-08-142-368A-18	Sequence 18, Appl
4	225	100.0	225	3	US-08-967-727-18	Sequence 18, Appl
5	225	100.0	225	4	US-08-037-230D-18	Sequence 18, Appl
6	157	69.8	945	4	US-09-056-105-7	Sequence 7, Appli
7	157	69.8	1019	4	US-09-056-105-13	Sequence 13, Appl
8	157	69.8	1375	2	US-08-993-738A-2	Sequence 2, Appli
9	157	69.8	1375	4	US-08-713-354C-2	Sequence 2, Appli
10	74	32.9	1640	1	US-07-807-043B-11	Sequence 11, Appl
11	74	32.9	1640	1	US-08-299-849B-11	Sequence 11, Appl
12	74	32.9	1640	2	US-08-142-368A-11	Sequence 11, Appl
13	74	32.9	1640	3	US-08-967-727-11	Sequence 11, Appl
14	74	32.9	1640	4	US-08-037-230D-11	Sequence 11, Appl
15	74	32.9	4204	2	US-08-928-615-1	Sequence 1, Appli
16	74	32.9	4204	4	US-09-056-105-6	Sequence 6, Appli
17	74	32.9	4204	4	US-09-166-448-1	Sequence 1, Appli
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19	36	16.0	4157	1	US-08-299-849B-9	Sequence 9, Appli
20	36	16.0	4157	2	US-08-142-368A-9	Sequence 9, Appli
21	36	16.0	4157	3	US-08-967-727-9	Sequence 9, Appli
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23	36	16.0	4559	4	US-09-056-105-5	Sequence 5, Appli
24	27	12.0	27	1	US-07-938-334C-18	Sequence 18, Appl
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28	27	12.0	27	4	US-08-393-273E-9	Sequence 9, Appli
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79	18	8.0	4031	3	US-08-845-528C-1	Sequence 1, Appli
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	118	16	7.1	2531	3	US-08-967-727-13	Sequence 13, Appl
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	132	16	7.1	4808	4	US-08-940-035A-10	Sequence 10, Appl
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	136	16	7.1	11495	4	US-09-056-105-9	Sequence 9, Appli
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	139	15	6.7	716	4	US-08-998-416-852	Sequence 852, App
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	159	15	6.7	3510	4	US-09-056-105-16	Sequence 16, Appl
c	160	15	6.7	3707	4	US-09-276-531-42	Sequence 42, Appl
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	165	15	6.7	6645	2	US-08-895-628-4	Sequence 4, Appli
c	166	15	6.7	8174	1	US-07-914-281-5	Sequence 5, Appli
c	167	15	6.7	8174	1	US-08-393-246-5	Sequence 5, Appli
c	168	15	6.7	8174	1	US-08-525-058A-5	Sequence 5, Appli
c	169	15	6.7	8174	2	US-08-696-731-5	Sequence 5, Appli
c	170	15	6.7	8174	4	US-09-042-531-5	Sequence 5, Appli
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c	173	15	6.7	8453	4	US-09-167-681-45	Sequence 45, Appl
c	174	15	6.7	10163	2	US-08-659-251-1	Sequence 1, Appli
c	175	15	6.7	10163	4	US-09-256-490-1	Sequence 1, Appli
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	177	15	6.7	36519	3	US-08-923-137-2	Sequence 2, Appli
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	179	14	6.2	50	1	US-08-620-467A-19	Sequence 19, Appl
	180	14	6.2	50	1	US-08-348-572-20	Sequence 20, Appl
	181	14	6.2	50	3	US-09-041-090B-20	Sequence 20, Appl
	182	14	6.2	81	3	US-08-963-121C-10	Sequence 10, Appl
	183	14	6.2	81	4	US-09-543-513-10	Sequence 10, Appl
	184	14	6.2	81	5	PCT-US95-04803-11	Sequence 11, Appl
	185	14	6.2	223	4	US-08-205-697A-14	Sequence 14, Appl
	186	14	6.2	223	4	US-08-702-525-14	Sequence 14, Appl
	187	14	6.2	223	5	PCT-US95-02576-14	Sequence 14, Appl
	188	14	6.2	231	4	US-09-328-111-287	Sequence 287, App
c	189	14	6.2	242	3	US-08-577-081A-2	Sequence 2, Appli
c	190	14	6.2	339	4	US-09-056-556-240	Sequence 240, App
	191	14	6.2	530	2	US-08-757-036-2	Sequence 2, Appli
	192	14	6.2	543	4	US-08-862-124-1	Sequence 1, Appli
c	193	14	6.2	543	4	US-08-862-124-3	Sequence 3, Appli
	194	14	6.2	633	4	US-09-230-637-2	Sequence 2, Appli
c	195	14	6.2	647	4	US-09-328-111-475	Sequence 475, App
	196	14	6.2	687	1	US-08-403-388-4	Sequence 4, Appli
	197	14	6.2	687	1	US-08-658-578-4	Sequence 4, Appli
	198	14	6.2	687	3	US-08-846-111D-4	Sequence 4, Appli
c	199	14	6.2	693	4	US-09-187-789-8	Sequence 8, Appli
c	200	14	6.2	764	4	US-09-392-014-3	Sequence 3, Appli
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	202	14	6.2	791	4	US-09-051-696-5	Sequence 5, Appli
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	205	14	6.2	973	1	US-07-805-123C-8	Sequence 8, Appli
	206	14	6.2	973	1	US-08-033-081B-8	Sequence 8, Appli
	207	14	6.2	973	3	US-09-013-881-16	Sequence 16, Appl
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	209	14	6.2	985	4	US-09-056-556-182	Sequence 182, App
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	211	14	6.2	1017	4	US-08-793-634B-6	Sequence 6, Appli
c	212	14	6.2	1062	4	US-09-067-800-1	Sequence 1, Appli
c	213	14	6.2	1062	4	US-09-105-652-1	Sequence 1, Appli
c	214	14	6.2	1062	4	US-09-349-677-1	Sequence 1, Appli
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	216	14	6.2	1107	2	US-08-142-368A-23	Sequence 23, Appl
	217	14	6.2	1107	3	US-08-967-727-23	Sequence 23, Appl
	218	14	6.2	1107	4	US-08-037-230D-23	Sequence 23, Appl
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	220	14	6.2	1261	4	US-08-702-525-12	Sequence 12, Appl
	221	14	6.2	1261	5	PCT-US95-02576-12	Sequence 12, Appl
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c	223	14	6.2	1414	1	US-08-476-000-62	Sequence 62, Appl
c	224	14	6.2	1414	1	US-08-472-840-62	Sequence 62, Appl
c	225	14	6.2	1414	2	US-08-476-976-62	Sequence 62, Appl
c	226	14	6.2	1414	3	US-08-474-410-62	Sequence 62, Appl
c	227	14	6.2	1414	4	US-08-486-673B-62	Sequence 62, Appl
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	230	14	6.2	1705	4	US-09-269-040-4	Sequence 4, Appli
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	232	14	6.2	1796	4	US-09-182-983-17	Sequence 17, Appl
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	239	14	6.2	1845	4	US-09-182-983-5	Sequence 5, Appli
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	241	14	6.2	1985	4	US-09-420-915-17	Sequence 17, Appl
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	263	14	6.2	2483	3	US-08-258-287B-34	Sequence 34, Appl
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	266	14	6.2	2548	2	US-08-855-213-41	Sequence 41, Appl
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	268	14	6.2	2553	1	US-08-236-410-1	Sequence 1, Appli
	269	14	6.2	2553	1	US-08-465-421-1	Sequence 1, Appli
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c	273	14	6.2	2610	1	US-08-644-271-28	Sequence 28, Appl
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c	275	14	6.2	2756	1	US-08-187-793-1	Sequence 1, Appli
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	290	14	6.2	3588	1	US-08-459-214-32	Sequence 32, Appl
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	312	14	6.2	7653	3	US-08-258-287B-1	Sequence 1, Appli
	313	14	6.2	7653	3	US-08-368-704C-1	Sequence 1, Appli
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c	319	14	6.2	9515	1	US-08-362-577C-13	Sequence 13, Appl
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	328	14	6.2	14042	4	US-08-652-877-85	Sequence 85, Appl
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	330	14	6.2	14080	4	US-08-652-877-87	Sequence 87, Appl
	331	14	6.2	14083	4	US-08-476-515A-83	Sequence 83, Appl
	332	14	6.2	14086	4	US-08-652-877-83	Sequence 83, Appl
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c	334	14	6.2	35100	4	US-08-757-669A-17	Sequence 17, Appl
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	344	13	5.8	15	4	US-09-081-646-783	Sequence 783, App
	345	13	5.8	18	4	US-08-618-957A-18	Sequence 18, Appl
	346	13	5.8	19	4	US-08-974-549A-449	Sequence 449, App
	347	13	5.8	20	1	US-08-199-510-2	Sequence 2, Appli
	348	13	5.8	20	2	US-08-628-422-2	Sequence 2, Appli
	349	13	5.8	20	4	US-09-433-694-78	Sequence 78, Appl
	350	13	5.8	20	5	PCT-US95-02082-2	Sequence 2, Appli
	351	13	5.8	21	4	US-08-793-701-10	Sequence 10, Appl
	352	13	5.8	24	4	US-08-789-329C-17	Sequence 17, Appl
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	356	13	5.8	25	3	US-08-737-607-25	Sequence 25, Appl
	357	13	5.8	25	5	PCT-US95-02082-1	Sequence 1, Appli
	358	13	5.8	27	1	US-07-766-351-9	Sequence 9, Appli
	359	13	5.8	27	1	US-07-938-334C-15	Sequence 15, Appl
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	361	13	5.8	27	1	US-08-073-103A-6	Sequence 6, Appli
	362	13	5.8	27	1	US-08-443-341-6	Sequence 6, Appli
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	364	13	5.8	27	3	US-08-354-679C-6	Sequence 6, Appli
	365	13	5.8	27	3	US-08-985-162-1107	Sequence 1107, Ap
	366	13	5.8	27	4	US-08-393-273E-6	Sequence 6, Appli
	367	13	5.8	27	5	PCT-US91-07290-9	Sequence 9, Appli
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	374	13	5.8	42	4	US-09-458-481B-1	Sequence 1, Appli
	375	13	5.8	60	3	US-08-918-406-5	Sequence 5, Appli
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	382	13	5.8	216	4	US-09-220-528-57	Sequence 57, Appl
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c	386	13	5.8	339	4	US-09-199-637A-258	Sequence 258, App
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c	389	13	5.8	350	3	US-09-124-698-35	Sequence 35, Appl
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	392	13	5.8	360	4	US-09-439-313-438	Sequence 438, App

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	395	13	5.8	373	2	US-08-976-074-3	Sequence 3, Appli
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	397	13	5.8	373	4	US-08-976-166A-3	Sequence 3, Appli
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	411	13	5.8	540	4	US-08-744-419-1	Sequence 1, Appli
	412	13	5.8	558	4	US-09-220-528-43	Sequence 43, Appl
	413	13	5.8	572	4	US-09-328-111-293	Sequence 293, App
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	437	13	5.8	718	4	US-08-998-416-832	Sequence 832, App
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	439	13	5.8	731	4	US-08-998-416-966	Sequence 966, App
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c 546	13	5.8	1776	4	US-08-753-247-17	Sequence 17, Appl
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c 667	13	5.8	2794	2	US-08-694-865-5	Sequence 5, Appli
c 668	13	5.8	2794	2	US-08-878-748-5	Sequence 5, Appli
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681	13	5.8	2882	4	US-09-608-285A-54	Sequence 54, Appl
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699	13	5.8	2991	2	US-08-384-616-49	Sequence 49, Appl
700	13	5.8	2991	2	US-08-904-686A-49	Sequence 49, Appl
701	13	5.8	2991	4	US-09-315-850-49	Sequence 49, Appl
702	13	5.8	2992	1	US-07-718-575-1	Sequence 1, Appli
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c 706	13	5.8	3010	4	US-09-199-637A-168	Sequence 168, App
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c 710	13	5.8	3116	1	US-08-149-103-2	Sequence 2, Appli
c 711	13	5.8	3116	1	US-08-451-883-2	Sequence 2, Appli
c 712	13	5.8	3117	3	US-08-909-954-3	Sequence 3, Appli
713	13	5.8	3164	1	US-08-188-228-49	Sequence 49, Appl
714	13	5.8	3164	1	US-08-332-643-43	Sequence 43, Appl
715	13	5.8	3164	1	US-08-332-638-49	Sequence 49, Appl
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721	13	5.8	3234	1	US-08-264-534-31	Sequence 31, Appl
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723	13	5.8	3234	1	US-08-465-500-31	Sequence 31, Appl
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725	13	5.8	3234	3	US-08-532-384-10	Sequence 10, Appl
726	13	5.8	3234	3	US-08-893-828-31	Sequence 31, Appl
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728	13	5.8	3243	2	US-08-468-579B-6	Sequence 6, Appli
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732	13	5.8	3282	1	US-08-486-270-11	Sequence 11, Appl
733	13	5.8	3282	3	US-08-367-264-11	Sequence 11, Appl
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783	13	5.8	3931	3	US-08-426-243-21	Sequence 21, Appl
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788	13	5.8	4015	4	US-08-854-050-224	Sequence 224, App
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c 796	13	5.8	4027	4	US-09-192-435-4	Sequence 4, Appli
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798	13	5.8	4029	4	US-08-974-549A-292	Sequence 292, App
799	13	5.8	4029	4	US-08-854-050-173	Sequence 173, App
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c 802	13	5.8	4031	3	US-08-845-528C-1	Sequence 1, Appli
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862	13	5.8	6063	2	US-08-788-279-4	Sequence 4, Appli
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871	13	5.8	6619	2	US-08-683-007A-3	Sequence 3, Appli
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c 886	13	5.8	7106	5	PCT-US95-01087-8	Sequence 8, Appli
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898	13	5.8	7863	2	US-08-384-616-35	Sequence 35, Appl
899	13	5.8	7863	2	US-08-904-686A-35	Sequence 35, Appl
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914	13	5.8	8910	3	US-08-582-776C-19	Sequence 19, Appl
915	13	5.8	8910	3	US-08-434-831B-19	Sequence 19, Appl
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922	13	5.8	9278	1	US-08-477-407-9	Sequence 9, Appli
923	13	5.8	9278	1	US-08-484-355-9	Sequence 9, Appli
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927	13	5.8	9416	2	US-08-904-686A-1	Sequence 1, Appli
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937	13	5.8	10962	3	US-09-079-587-6	Sequence 6, Appli
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942	13	5.8	11558	5	PCT-US93-06251-23	Sequence 23, Appl
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c 957	13	5.8	17612	4	US-09-479-453-29	Sequence 29, Appl
958	13	5.8	18609	4	US-08-943-731-1	Sequence 1, Appli
959	13	5.8	19877	2	US-08-816-155B-8	Sequence 8, Appli
960	13	5.8	19877	3	US-09-079-587-8	Sequence 8, Appli
c 961	13	5.8	20303	1	US-08-370-975B-6	Sequence 6, Appli
c 962	13	5.8	21126	1	US-08-008-216-19	Sequence 19, Appl
c 963	13	5.8	21126	1	US-08-459-569-19	Sequence 19, Appl
c 964	13	5.8	21126	1	US-08-458-831-19	Sequence 19, Appl
c 965	13	5.8	26764	1	US-08-370-975B-1	Sequence 1, Appli
966	13	5.8	28720	4	US-09-341-587-7	Sequence 7, Appli
c 967	13	5.8	31571	1	US-08-323-443B-1	Sequence 1, Appli
c 968	13	5.8	34446	4	US-09-103-330-35	Sequence 35, Appl
969	13	5.8	38682	4	US-08-943-731-2	Sequence 2, Appli
970	13	5.8	42235	4	US-09-199-637A-1	Sequence 1, Appli
971	13	5.8	43795	3	US-08-742-185-101	Sequence 101, App
972	13	5.8	49136	4	US-09-422-869-1	Sequence 1, Appli
c 973	13	5.8	49136	4	US-09-422-869-1	Sequence 1, Appli
c 974	13	5.8	50341	1	US-08-247-901C-1	Sequence 1, Appli
c 975	13	5.8	50341	2	US-09-075-904-1	Sequence 1, Appli
976	13	5.8	50937	4	US-09-428-517-1	Sequence 1, Appli

c 977	13	5.8	52297	4	US-09-426-436-1	Sequence 1, Appli
c 978	13	5.8	52297	4	US-08-705-557-1	Sequence 1, Appli
c 979	13	5.8	53526	3	US-08-658-136-2	Sequence 2, Appli
c 980	13	5.8	53577	3	US-08-658-136-1	Sequence 1, Appli
c 981	13	5.8	56516	2	US-08-996-306-1	Sequence 1, Appli
c 982	13	5.8	56516	4	US-09-338-907-1	Sequence 1, Appli
c 983	13	5.8	56516	4	US-09-218-207-1	Sequence 1, Appli
c 984	13	5.8	56520	4	US-09-338-907-179	Sequence 179, App
c 985	13	5.8	56520	4	US-09-218-207-179	Sequence 179, App
986	13	5.8	59065	4	US-09-813-817-3	Sequence 3, Appli
987	13	5.8	84495	4	US-09-797-906-3	Sequence 3, Appli
c 988	13	5.8	84495	4	US-09-797-906-3	Sequence 3, Appli
c 989	13	5.8	152331	3	US-09-128-155-16	Sequence 16, Appl
990	13	5.8	176373	3	US-09-128-155-17	Sequence 17, Appl
991	13	5.8	246240	2	US-08-724-394A-20	Sequence 20, Appl
992	13	5.8	246240	2	US-08-724-394A-21	Sequence 21, Appl
993	13	5.8	246240	2	US-08-724-394A-22	Sequence 22, Appl
c 994	13	5.8	4411529	4	US-09-103-840A-1	Sequence 1, Appli
c 995	12	5.3	15	1	US-08-122-433-43	Sequence 43, Appl
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c 998	12	5.3	17	4	US-08-584-040-4055	Sequence 4055, Ap
999	12	5.3	18	4	US-08-584-040-3031	Sequence 3031, Ap
1000	12	5.3	20	1	US-08-260-515-14	Sequence 14, Appl

ALIGNMENTS

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RESULT   1
US-07-807-043B-15
; Sequence 15, Application US/07807043B
; Patent No. 5342774
;  GENERAL INFORMATION:
;    APPLICANT:  Boon, Thierry, Van den Eynde, Beno t
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
;    TITLE OF INVENTION:  Rejection Antigens and Uses Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/807,043B
;      FILING DATE:  19911212
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      FILING DATE:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-May-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5342774man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 253.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  225 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  singular
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  MAGE-6 gene
US-07-807-043B-15


  Query Match           100.0%;  Score 225;  DB 1;  Length 225;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-103;
  Matches  225;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAGGACAGGCTTCCTGATAATC 180
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RESULT   2
US-08-299-849B-18
; Sequence 18, Application US/08299849B
; Patent No. 5612201
;  GENERAL INFORMATION:
;    APPLICANT:  De Plaen, Etienne; Boon-Falleur, Thierry;
;    APPLICANT:  Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
;    APPLICANT:  Chomez, Patrick
;    TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Useful In
;    TITLE OF INVENTION:  Determining Expression Of A Tumor Antigen Precursor
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/299,849B
;      FILING DATE:  1-SEPTEMBER-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/037,230
;      FILING DATE:  26-MARCH-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/04354
;      FILING DATE:  22-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/807,043
;      FILING DATE:  12-DECEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      APPLICATION NUMBER:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-May-1991
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5612201man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5355
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  225 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  MAGE-6 gene
US-08-299-849B-18


  Query Match             100.0%;  Score 225;  DB 1;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-103;
  Matches  225;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TATTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
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Qy      61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
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RESULT   3
US-08-142-368A-18
; Sequence 18, Application US/08142368A
; Patent No. 5925729
;  GENERAL INFORMATION:
;    APPLICANT:  Boon-Falleur, Thierry; Van der Bruggen, Thierry;
;    APPLICANT:  Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
;    APPLICANT:  Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
;    TITLE OF INVENTION:  Rejection Antigens and Uses Thereof
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,368A
;      FILING DATE:  02-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/04354
;      FILING DATE:  22-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/807,043
;      FILING DATE:  12-DECEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      APPLICATION NUMBER:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-May-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5925729man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5253.4-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  225 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  MAGE-6 gene
US-08-142-368A-18


  Query Match             100.0%;  Score 225;  DB 2;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-103;
  Matches  225;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
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Qy     121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAGGACAGGCTTCCTGATAATC 180
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Qy     181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCTGAGGAG 225
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RESULT   4
US-08-967-727-18
; Sequence 18, Application US/08967727
; Patent No. 6025474
;  GENERAL INFORMATION:
;    APPLICANT:  Gaugler, B atrice; Van den Eynde, Beno t;
;    APPLICANT:  van der Bruggen, Pierre;  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Coding For
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/967,727
;      FILING DATE:
;      CLASSIFICATION:  435
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/037,230
;      FILING DATE:  26-MARCH-1993
;      APPLICATION NUMBER:  PCT/US92/04354
;      FILING DATE:  22-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/807,043
;      FILING DATE:  12-DECEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,365
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      FILING DATE:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6025474man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5353
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  225 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  MAGE-6 gene
US-08-967-727-18


  Query Match             100.0%;  Score 225;  DB 3;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-103;
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Db      1 TATTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60

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RESULT   5
US-08-037-230D-18
; Sequence 18, Application US/08037230D
; Patent No. 6235525
;  GENERAL INFORMATION:
;    APPLICANT:  Gaugler, B atrice; Van den Eynde, Beno t;
;    APPLICANT:  van der Bruggen, Pierre;  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Coding For
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/037,230D
;      FILING DATE:  26-MARCH-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/04354
;      FILING DATE:  22-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/807,043
;      FILING DATE:  12-DECEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      FILING DATE:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6235525man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5353
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  225 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  MAGE-6 gene
US-08-037-230D-18


  Query Match             100.0%;  Score 225;  DB 4;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-103;
  Matches  225;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TATTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
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Qy     61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
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Qy    121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAGGACAGGCTTCCTGATAATC 180
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Db    121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAGGACAGGCTTCCTGATAATC 180

Qy    181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCTGAGGAG 225
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RESULT   6
US-09-056-105-7
; Sequence 7, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
;  APPLICANT: KIPPS, THOMAS J.
;  APPLICANT: WU, YUNQI
;  TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
;  TITLE OF INVENTION: PROCESSING
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;  FILE REFERENCE: 233/221
;  CURRENT APPLICATION NUMBER: US/09/056,105
;  CURRENT FILING DATE: 1998-04-06
;  EARLIER APPLICATION NUMBER: 60/043,467
;  EARLIER FILING DATE: 1997-04-10
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 945
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-056-105-7


  Query Match             69.8%;  Score 157;  DB 4;  Length 945;
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Db     436 ttctttcctgtgatcttcagcaaagcttccgattccttgcagctggtctttggcatcgag 495

Qy      64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     496 ctgatggaagtggaccccatcggccacgtgtacatctttgccacctgcctgggcctctcc 555

Qy     124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
           |||||||||||||||||||||||||||||||||||||
Db     556 tacgatggcctgctgggtgacaatcagatcatgccca 592


RESULT   7
US-09-056-105-13
; Sequence 13, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
;  APPLICANT: KIPPS, THOMAS J.
;  APPLICANT: WU, YUNQI
;  TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
;  TITLE OF INVENTION: PROCESSING
;  FILE REFERENCE: 233/221
;  CURRENT APPLICATION NUMBER: US/09/056,105
;  CURRENT FILING DATE: 1998-04-06
;  EARLIER APPLICATION NUMBER: 60/043,467
;  EARLIER FILING DATE: 1997-04-10
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 1019
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-056-105-13


  Query Match             69.8%;  Score 157;  DB 4;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-69;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     501 ttctttcctgtgatcttcagcaaagcttccgattccttgcagctggtctttggcatcgag 560

Qy      64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     561 ctgatggaagtggaccccatcggccacgtgtacatctttgccacctgcctgggcctctcc 620

Qy     124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
           |||||||||||||||||||||||||||||||||||||
Db     621 tacgatggcctgctgggtgacaatcagatcatgccca 657


RESULT   8
US-08-993-738A-2
; Sequence 2, Application US/08993738A
; Patent No. 5928938
;  GENERAL INFORMATION:
;    APPLICANT:  van der Bruggen, Pierre; DePlaen Etienne;
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  Isolated Peptides Which Complex With
;    TITLE OF INVENTION:  HLA-Cw*16 Molecules, and Uses Thereof
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY: USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/993,738A
;      FILING DATE:  19-December-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/713,354
;      FILING DATE:  13-September-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5928938man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5460.1 DIV - JEL/NDH
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1375 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-993-738A-2


  Query Match             69.8%;  Score 157;  DB 2;  Length 1375;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-69;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     595 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 654

Qy      64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     655 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 714

Qy     124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
           |||||||||||||||||||||||||||||||||||||
Db     715 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 751


RESULT   9
US-08-713-354C-2
; Sequence 2, Application US/08713354C
; Patent No. 6265215
;  GENERAL INFORMATION:
;    APPLICANT:  van der Bruggen, Pierre; DePlaen Etienne;
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  Isolated Peptides Which Complex With
;    TITLE OF INVENTION:  HLA-Cw*16 Molecules, and Uses Thereof
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
```

```
;       STREET:  805 Third Avenue
;       CITY:  New York City
;       STATE:  New York
;       ZIP:  10022
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;       COMPUTER:  IBM
;       OPERATING SYSTEM:  PC-DOS
;       SOFTWARE:  Wordperfect
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/713,354C
;       FILING DATE:  13-September-1996
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Hanson, No. 6265215man D.
;       REGISTRATION NUMBER:  30,946
;       REFERENCE/DOCKET NUMBER:  LUD 5460
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 688-9200
;       TELEFAX:  (212) 838-3884
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1375 nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-713-354C-2


  Query Match             69.8%;  Score 157;  DB 4;  Length 1375;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-69;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     595 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 654

Qy      64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     655 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 714

Qy     124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
           |||||||||||||||||||||||||||||||||||||
Db     715 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 751


RESULT  10
US-07-807-043B-11
; Sequence 11, Application US/07807043B
; Patent No. 5342774
;  GENERAL INFORMATION:
;    APPLICANT:  Boon, Thierry, Van den Eynde, Beno t
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
;    TITLE OF INVENTION:  Rejection Antigens and Uses Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/807,043B
;      FILING DATE:  19911212
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      FILING DATE:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-May-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5342774man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 253.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1640 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  singular
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    FEATURE:
;      NAME/KEY:  cDNA MAGE-3
US-07-807-043B-11


  Query Match             32.9%;  Score 74;  DB 1;  Length 1640;
  Best Local Similarity   99.2%;  Pred. No. 5.4e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     639 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGTA 698

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     699 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 758

Qy     156 GCCCA 160
           |||||
Db     759 GCCCA 763


RESULT  11
US-08-299-849B-11
; Sequence 11, Application US/08299849B
; Patent No. 5612201
;  GENERAL INFORMATION:
;    APPLICANT:  De Plaen, Etienne; Boon-Falleur, Thierry;
;    APPLICANT:  Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
;    APPLICANT:  Chomez, Patrick
;    TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Useful In
;    TITLE OF INVENTION:  Determining Expression Of A Tumor Antigen Precursor
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/299,849B
;      FILING DATE:  1-SEPTEMBER-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/037,230
;      FILING DATE:  26-MARCH-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/04354
```

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;      FILING DATE:  22-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/807,043
;      FILING DATE:  12-DECEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      APPLICATION NUMBER:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-May-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5612201man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5355
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1640 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    FEATURE:
;      NAME/KEY:  cDNA MAGE-3
US-08-299-849B-11


  Query Match             32.9%;  Score 74;  DB 1;  Length 1640;
  Best Local Similarity   99.2%;  Pred. No. 5.4e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     639 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGTA 698

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     699 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 758

Qy     156 GCCCA 160
           |||||
Db     759 GCCCA 763


RESULT  12
US-08-142-368A-11
; Sequence 11, Application US/08142368A
; Patent No. 5925729
;  GENERAL INFORMATION:
;    APPLICANT:  Boon-Falleur, Thierry; Van der Bruggen, Thierry;
;    APPLICANT:  Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
;    APPLICANT:  Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
;    TITLE OF INVENTION:  Rejection Antigens and Uses Thereof
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,368A
;      FILING DATE:  02-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/04354
;      FILING DATE:  22-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/807,043
;      FILING DATE:  12-DECEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      APPLICATION NUMBER:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-May-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5925729man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5253.4-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1640 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    FEATURE:
;      NAME/KEY:  cDNA MAGE-3
US-08-142-368A-11


  Query Match             32.9%;  Score 74;  DB 2;  Length 1640;
  Best Local Similarity   99.2%;  Pred. No. 5.4e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     639 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGTA 698

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     699 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 758

Qy     156 GCCCA 160
           |||||
Db     759 GCCCA 763


RESULT  13
US-08-967-727-11
; Sequence 11, Application US/08967727
; Patent No. 6025474
;  GENERAL INFORMATION:
;    APPLICANT:  Gaugler, B atrice; Van den Eynde, Beno t;
;    APPLICANT:  van der Bruggen, Pierre;  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Coding For
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
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;       SOFTWARE:  Wordperfect
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/967,727
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/037,230
;       FILING DATE:  26-MARCH-1993
;       APPLICATION NUMBER:  PCT/US92/04354
;       FILING DATE:  22-MAY-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/807,043
;       FILING DATE:  12-DECEMBER-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/764,365
;       FILING DATE:  23-SEPTEMBER-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/728,838
;       FILING DATE:  9-JULY-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/705,702
;       FILING DATE:  23-MAY-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Hanson, No. 6025474man D.
;       REGISTRATION NUMBER:  30,946
;       REFERENCE/DOCKET NUMBER:  LUD 5353
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 688-9200
;       TELEFAX:  (212) 838-3884
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1640 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     FEATURE:
;       NAME/KEY:  cDNA MAGE-3
US-08-967-727-11


  Query Match             32.9%;  Score 74;  DB 3;  Length 1640;
  Best Local Similarity   99.2%;  Pred. No. 5.4e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     639 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGTA 698

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     699 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 758

Qy     156 GCCCA 160
           |||||
Db     759 GCCCA 763


RESULT  14
US-08-037-230D-11
; Sequence 11, Application US/08037230D
; Patent No. 6235525
;  GENERAL INFORMATION:
;    APPLICANT:  Gaugler, B atrice; Van den Eynde, Beno t;
;    APPLICANT:  van der Bruggen, Pierre;  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Coding For
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/037,230D
;      FILING DATE:  26-MARCH-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/04354
;      FILING DATE:  22-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/807,043
;      FILING DATE:  12-DECEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      FILING DATE:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6235525man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5353
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1640 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    FEATURE:
;      NAME/KEY:  cDNA MAGE-3
US-08-037-230D-11


  Query Match             32.9%;  Score 74;  DB 4;  Length 1640;
  Best Local Similarity   99.2%;  Pred. No. 5.4e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     639 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGTA 698

Qy      96 CATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCAT 155
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RESULT  15
US-08-928-615-1
; Sequence 1, Application US/08928615
; Patent No. 5965535
;  GENERAL INFORMATION:
;    APPLICANT:  Chaux, Pascal
;    APPLICANT:  Stroobant, Vincent
;    APPLICANT:  Boon, Thierry
;    APPLICANT:  van der Bruggen, Pierre
;    TITLE OF INVENTION:  MAGE-3 PEPTIDES PRESENTED
;    TITLE OF INVENTION:  BY HLA CLASS II MOLECULES
;    NUMBER OF SEQUENCES:  13
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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/928,615
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4204 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  2465...3406
US-08-928-615-1


  Query Match            32.9%;  Score 74;  DB 2;  Length 4204;
  Best Local Similarity  99.2%;  Pred. No. 5.3e-28;
  Matches  124;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Search completed: May 24, 2002, 03:44:52
Job time: 4446 sec
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 01:34:31 ; Search time 2080.58 Seconds
(without alignments)
1459.600 Million cell updates/sec

Title: US-08-037-230D-18
Perfect score: 225
Sequence: 1 TATTTCTTTCCTGTGATCTT.....GCGACTGTGCCCCTGAGGAG 225

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : EST:*
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2: em_esthum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AA984439 am86d08.s
AQ943234 Sheared D
BF229613 RC2-CS001
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253	17	7.6	438	10	BE489637	BE489637 WHE1071-1
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267	17	7.6	456	9	AI305255	AI305255 qm08e02.x
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279	17	7.6	484	9	AV747231	AV747231 AV747231
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281	17	7.6	488	12	AQ405792	AQ405792 HS_5081_A
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295	17	7.6	523	12	AQ669596	AQ669596 HS_5422_B
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	414	17	7.6	914	12	CNS04LP1 AL296398 Tetraodon
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	418	17	7.6	946	12	CNS03MSG AL251161 Tetraodon
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	477	16	7.1	266	9	AV327463 AV327463 AV327463
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	855	16	7.1	693	9	BE037730	BE037730 AA03D05 A
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	923	16	7.1	877	10	BG973247	BG973247 602842610
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980	16	7.1	1111	10	BG114803	BG114803 602315246
981	16	7.1	1111	10	BM479073	BM479073 AGENCOURT
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993	15	6.7	85	9	AA038939	AA038939 mi97b08.r
994	15	6.7	101	10	BI344833	BI344833 373426 MA
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997	15	6.7	114	12	AZ376748	AZ376748 1M0130E16
998	15	6.7	115	10	BI059013	BI059013 RC4-GN027
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ALIGNMENTS

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ACCESSION   BG477228
VERSION     BG477228.1  GI:13409507
KEYWORDS    EST.
SOURCE      human.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1411  row: i  column: 10
            High quality sequence stop: 499.
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                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
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ACCESSION   BI086876
VERSION     BI086876.1  GI:14505206
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 768)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11010  row: k  column: 24
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BASE COUNT      170 a    227 c    212 g    158 t      1 others
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RESULT   3
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DEFINITION  602524881F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642868 5',
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VERSION     BG476912.1  GI:13409178
KEYWORDS    EST.
SOURCE      human.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 776)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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                     /clone="IMAGE:4642868"
                     /clone_lib="NIH_MGC_20"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      180 a    197 c    232 g    167 t
ORIGIN


  Query Match            69.8%;  Score 157;  DB 10;  Length 776;
  Best Local Similarity  100.0%;  Pred. No. 5.6e-70;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 253

Qy     64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 313

Qy    124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
          ||||||||||||||||||||||||||||||||||||
Db    314 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 350


RESULT   4
BG397171
LOCUS       BG397171                878 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  602434130F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4552086 5',
            mRNA sequence.
ACCESSION   BG397171
VERSION     BG397171.1  GI:13290619
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 878)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1247  row: l  column: 07
            High quality sequence stop: 866.
FEATURES             Location/Qualifiers
     source          1. .878
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4552086"
                     /clone_lib="NIH_MGC_20"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      197 a    214 c    262 g    205 t
ORIGIN


  Query Match            69.8%;  Score 157;  DB 10;  Length 878;
  Best Local Similarity  100.0%;  Pred. No. 5.8e-70;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 252

Qy     64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 312

Qy    124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
          ||||||||||||||||||||||||||||||||||||
Db    313 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 349


RESULT   5
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BG476078
LOCUS       BG476078                886 bp    mRNA    linear   EST 21-MAR-2001
DEFINITION  602520963F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4639670 5',
            mRNA sequence.
ACCESSION   BG476078
VERSION     BG476078.1  GI:13408357
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 886)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1403  row: m  column: 15
            High quality sequence stop: 730.
FEATURES             Location/Qualifiers
     source          1. .886
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4639670"
                     /clone_lib="NIH_MGC_20"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      183 a    231 c    262 g    210 t
ORIGIN
```

```
  Query Match             69.8%;  Score 157;  DB 10;  Length 886;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-70;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     97 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 156

Qy     64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    157 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 216

Qy    124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
          |||||||||||||||||||||||||||||||||||||
Db    217 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 253
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RESULT   6
BG765817
LOCUS       BG765817                894 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602739647F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4869682 5',
            mRNA sequence.
ACCESSION   BG765817
VERSION     BG765817.1  GI:14076470
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 894)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1741  row: m  column: 11
            High quality sequence stop: 835.
FEATURES             Location/Qualifiers
     source          1. .894
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4869682"
                     /clone_lib="NIH_MGC_49"
                     /tissue_type="melanotic melanoma, high MDR (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library. |"
BASE COUNT      193 a    252 c    275 g    174 t
ORIGIN
```

```
  Query Match             69.8%;  Score 157;  DB 10;  Length 894;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-70;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    616 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 675

Qy     64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    676 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 735

Qy    124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
          |||||||||||||||||||||||||||||||||||||
Db    736 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 772
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RESULT   7
BG760839
LOCUS       BG760839                707 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602717006F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4840824 5',
            mRNA sequence.
ACCESSION   BG760839
VERSION     BG760839.1  GI:14071479
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 707)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
```

```
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1672  row: k  column: 01
            High quality sequence stop: 619.
FEATURES              Location/Qualifiers
     source           1. .707
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4840824"
                      /clone_lib="NIH_MGC_49"
                      /tissue_type="melanotic melanoma, high MDR (cell line)"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                      into EcoRI/XhoI sites using the following 5' adaptor:
                      GGCACGAG(G). Size-selected >500bp for average insert size
                      1.8kb. Library constructed by Ling Hong in the laboratory
                      of Gerald M. Rubin (University of California, Berkeley)
                      using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                      II RT (Life Technologies). Note: this is a NIH_MGC
                      Library. |"
BASE COUNT      145 a    241 c    186 g    135 t
ORIGIN


  Query Match             60.9%;  Score 137;  DB 10;  Length 707;
  Best Local Similarity   100.0%;  Pred. No. 1e-59;
  Matches  137;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    402 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 461

Qy     64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    462 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 521

Qy    124 TACGATGGCCTGCTGGG 140
          |||||||||||||||||
Db    522 TACGATGGCCTGCTGGG 538


RESULT  8
BF792356
LOCUS       BF792356                876 bp    mRNA    linear   EST 12-JAN-2001
DEFINITION  602252896F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4345222 5',
            mRNA sequence.
ACCESSION   BF792356
VERSION     BF792356.1  GI:12097410
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 876)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9964  row: p  column: 23
            High quality sequence stop: 780.
FEATURES              Location/Qualifiers
     source           1. .876
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4345222"
                      /clone_lib="NIH_MGC_84"
                      /tissue_type="adrenal cortex carcinoma, cell line"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
                      NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
                      primed. Average insert size 1.229 kb. Library enriched for
                      full-length clones and constructed by Life Technologies.
                      Note: this is a NIH_MGC Library."
BASE COUNT      185 a    215 c    248 g    228 t
ORIGIN


  Query Match             60.9%;  Score 137;  DB 10;  Length 876;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-59;
  Matches  137;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     24 CAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCAT 83
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 CAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCAT 160

Qy     84 CGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGA 143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 CGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGA 220

Qy    144 CAATCAGATCATGCCCA 160
          |||||||||||||||||
Db    221 CAATCAGATCATGCCCA 237


RESULT  9
BM470991
LOCUS       BM470991                1021 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6478212 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5562971
            5', mRNA sequence.
ACCESSION   BM470991
VERSION     BM470991.1  GI:18520033
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12293  row: d  column: 12
            High quality sequence stop: 725.
FEATURES              Location/Qualifiers
     source           1. .1021
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5562971"
                      /clone_lib="NIH_MGC_72"
                      /tissue_type="melanotic melanoma"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 2 kb.   Library constructed by Life
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                    Technologies."
BASE COUNT      232 a    290 c    292 g    206 t      1 others
ORIGIN


  Query Match             56.9%;  Score 128;  DB 10;  Length 1021;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-55;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     596 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 655

Qy      64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     656 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 715

Qy     124 TACGATGG 131
           ||||||||
Db     716 TACGATGG 723


RESULT  10
BE541476
LOCUS       BE541476                795 bp    mRNA    linear   EST 09-AUG-2000
DEFINITION  601067928F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454135 5',
            mRNA sequence.
ACCESSION   BE541476
VERSION     BE541476.1  GI:9770121
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 795)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8438  row: h  column: 08
            High quality sequence stop: 662.
FEATURES             Location/Qualifiers
     source          1. .795
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3454135"
                     /clone_lib="NIH_MGC_10"
                     /cell_line="MGC36"
                     /lab_host="DH10B"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5 kb. Library prepared by Life
                     Technologies."
BASE COUNT      182 a    199 c    234 g    180 t
ORIGIN


  Query Match             48.0%;  Score 108;  DB 10;  Length 795;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-45;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      53 TTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCC 112
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 TTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCC 297

Qy     113 TGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 TGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 345


RESULT  11
BE733003
LOCUS       BE733003                696 bp    mRNA    linear   EST 15-SEP-2000
DEFINITION  601569780F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3844482 5',
            mRNA sequence.
ACCESSION   BE733003
VERSION     BE733003.1  GI:10146995
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 696)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM540  row: p  column: 19
            High quality sequence stop: 693.
FEATURES             Location/Qualifiers
     source          1. .696
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3844482"
                     /clone_lib="NIH_MGC_21"
                     /tissue_type="choriocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                     for average insert size 1.8kb.  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      142 a    206 c    204 g    144 t
ORIGIN


  Query Match             46.2%;  Score 104;  DB 10;  Length 696;
  Best Local Similarity   100.0%;  Pred. No. 9.4e-43;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     560 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 619

Qy      64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCAC 107
           |||||||||||||||||||||||||||||||||||||||||||
Db     620 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCAC 663


RESULT  12
BG764972
LOCUS       BG764972                704 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602737745F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4863059 5',
            mRNA sequence.
ACCESSION   BG764972
VERSION     BG764972.1  GI:14075625
KEYWORDS    EST.
SOURCE      human.
```

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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 704)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1724  row: i  column: 12
            High quality sequence stop: 704.
FEATURES              Location/Qualifiers
     source           1. .704
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4863059"
                      /clone_lib="NIH_MGC_49"
                      /tissue_type="melanotic melanoma, high MDR (cell line)"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                      into EcoRI/XhoI sites using the following 5' adaptor:
                      GGCACGAG(G). Size-selected >500bp for average insert size
                      1.8kb. Library constructed by Ling Hong in the laboratory
                      of Gerald M. Rubin (University of California, Berkeley)
                      using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                      II RT (Life Technologies). Note: this is a NIH_MGC
                      Library. |"
BASE COUNT      145 a    214 c    200 g    145 t
ORIGIN


  Query Match             45.3%;  Score 102;  DB 10;  Length 704;
  Best Local Similarity   100.0%;  Pred. No. 1e-41;
  Matches  102;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      55 GGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTG 114
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     603 GGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTG 662

Qy     115 GGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATG 156
           ||||||||||||||||||||||||||||||||||||||||||
Db     663 GGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATG 704


RESULT  13
BE730893
LOCUS       BE730893                760 bp    mRNA    linear   EST 15-SEP-2000
DEFINITION  601570013F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3844707 5',
            mRNA sequence.
ACCESSION   BE730893
VERSION     BE730893.1  GI:10144885
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 760)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM541  row: j  column: 04
            High quality sequence stop: 742.
FEATURES              Location/Qualifiers
     source           1. .760
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:3844707"
                      /clone_lib="NIH_MGC_21"
                      /tissue_type="choriocarcinoma"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
                      Site_2: EcoRI; cDNA made by oligo-dT priming.
                      Directionally cloned into EcoRI/XhoI sites using the
                      following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                      for average insert size 1.8kb.  Library constructed by
                      Ling Hong in the laboratory of Gerald M. Rubin (University
                      of California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      166 a    220 c    216 g    158 t
ORIGIN


  Query Match             44.9%;  Score 101;  DB 10;  Length 760;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-41;
  Matches  101;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     545 TTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 604

Qy      64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGC 104
           |||||||||||||||||||||||||||||||||||||||||
Db     605 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGC 645


RESULT  14
BE734462
LOCUS       BE734462                1101 bp    mRNA    linear   EST 15-SEP-2000
DEFINITION  601566241F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841042 5',
            mRNA sequence.
ACCESSION   BE734462
VERSION     BE734462.1  GI:10148454
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM532  row: a  column: 11
            High quality sequence stop: 709.
FEATURES              Location/Qualifiers
     source           1. .1101
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                      /db_xref="taxon:9606"
                      /clone="IMAGE:3841042"
                      /clone_lib="NIH_MGC_21"
                      /tissue_type="choriocarcinoma"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
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Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 272 a 282 c 344 g 203 t
ORIGIN

Query Match 43.6%; Score 98; DB 10; Length 1101;
Best Local Similarity 100.0%; Pred. No. 1.2e-39;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATG 69
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 603 CCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATG 662

Qy 70 GAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCAC 107
|||||||||||||||||||||||||||||||||||||
Db 663 GAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCAC 700

RESULT 15
BG718421
LOCUS BG718421 768 bp mRNA linear EST 08-MAY-2001
DEFINITION 602696451F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4828429 5', mRNA sequence.
ACCESSION BG718421
VERSION BG718421.1 GI:13997608
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 768)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10746 row: f column: 14
High quality sequence stop: 759.
FEATURES Location/Qualifiers
source 1. .768
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4828429"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 154 a 225 c 236 g 152 t 1 others
ORIGIN

Query Match 41.3%; Score 93; DB 10; Length 768;
Best Local Similarity 100.0%; Pred. No. 4.3e-37;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 CAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCAT 83
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 649 CAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCAT 708

Qy 84 CGGCCACGTGTACATCTTTGCCACCTGCCTGGG 116
||||||||||||||||||||||||||||||||
Db 709 CGGCCACGTGTACATCTTTGCCACCTGCCTGGG 741

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